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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:07:24 ; Search time 17 Seconds
(without alignments)
1175.668 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREEDFETVGI.....KEICDYPFRQIAKWHVLCGD 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2201	100.0	425	1	SYT4_HUMAN
2	2006	91.1	425	1	SYT4_RAT
3	1988	90.3	425	1	SYT4_MOUSE
4	1167.5	53.0	430	1	SYTB_MOUSE
5	1162	52.8	431	1	SYTB_HUMAN
6	1156.5	52.5	430	1	SYTB_RAT
7	627.5	28.5	403	1	SYT7_MOUSE
8	623.5	28.3	474	1	SY65_DROME
9	615.5	28.0	402	1	SYT7_HUMAN
10	606.5	27.6	426	1	SY65_APLCA
11	604.5	27.5	422	1	SYT2_MOUSE
12	603.5	27.4	422	1	SYT2_RAT
13	594.5	27.0	537	1	SY63_DISOM
14	594	27.0	441	1	SYT1_CAEEL
15	592	26.9	498	1	SYTA_RAT
16	590	26.8	523	1	SYTA_MOUSE
17	581	26.4	421	1	SYT1_MOUSE
18	581	26.4	422	1	SYT1_BOVIN
19	581	26.4	422	1	SYT1_HUMAN
20	580.5	26.4	386	1	SYT5_MOUSE
21	580	26.4	421	1	SYT1_RAT
22	579.5	26.3	421	1	SY61_DISOM
23	575	26.1	424	1	SYT1_CHICK
24	574.5	26.1	439	1	SY62_DISOM
25	573.5	26.1	386	1	SYT5_HUMAN
26	571.5	26.0	386	1	SYT5_MOUSE
27	520	23.6	588	1	SYT3_RAT
28	518.5	23.6	590	1	SYT3_HUMAN
29	516	23.4	587	1	SYT3_MOUSE
30	408	18.5	704	1	RP3A_BOVIN
31	399.5	18.2	694	1	RP3A_HUMAN
32	394.5	17.9	681	1	RP3A_MOUSE
33	393.5	17.9	684	1	RP3A_RAT

34	361.5	16.4	395	1	SYTB_MOUSE
35	332	15.1	1021	1	YPT7_CAEEL
36	192.5	8.7	5120	1	PCLO_CHICK
37	184.5	8.4	5147	1	PCLO_HUMAN
38	181.5	8.2	5038	1	PCLO_MOUSE
39	180	8.2	5085	1	PCLO_RAT
40	179.5	8.2	682	1	KPCG_BOVIN
41	179.5	8.2	697	1	KPCG_RABIT
42	178.5	8.1	697	1	KPCG_HUMAN
43	177.5	8.1	697	1	KPCG_MOUSE
44	175	8.0	826	1	RS65_HUMAN
45	173.5	7.9	834	1	RS63_BOVIN

Q9r0n6	mus musculus
P41885	caenorhabditis
Q9pu36	gallus gallus
Q9y6v0	homo sapien
Q9gyx7	mus musculus
Q9jks6	rattus norv
P05128	bos taurus
P10829	oryctolagus
P05129	homo sapien
P05697	mus musculus
Q43374	homo sapien
Q28013	bos taurus

ALIGNMENTS

RESULT 1

SYT4_HUMAN

ID SYT4_HUMAN STANDARD; PRT; 425 AA.

AC Q9H2E2; Q9P2K4; DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Synaptotagmin IV (SyTIV).

GN SYT4 OR KIAA1342.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20538435; PubMed=10938284;

RA Ferguson G.D., Chen X.-N., Korenberg J.R., Herschman H.R.;

RT "The human synaptotagmin IV gene defines an evolutionary break point

between syntenic mouse and human chromosome regions but retains

ligand inducibility and tissue specificity.";

RL J. Biol. Chem. 275:36920-36926(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=20181126; PubMed=10718198;

RA Nagase T., Kikuno R., Ishikawa K.-I., Hirotsawa M., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XVI.

The complete sequences of 150 new cDNA clones from brain which code

for large proteins in vitro.";

RL DNA Res. 7:65-73(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R., Touchman J.W., Green E.D., Dickinson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,

Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of

secretory vesicles through Ca(2+) and phospholipid binding to the

CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
 CC vesicles.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN. WITHIN BRAIN, EXPRESSION
 CC IS HIGHEST IN HIPPOCAMPUS, WITH SUBSTANTIAL LEVELS ALSO DETECTED
 CC IN AMYGDALA AND THALAMUS.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
 CC
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 CC
 CC EMBL; AF299075; AAG37229.1; -;
 CC EMBL; AB037763; BAA92580.1; ALT_INIT.
 CC EMBL; BC036538; AAH36538.1; -;
 CC HSP; P21707; 1BYN.
 CC Genew; HGNC:11512; SYT4.
 CC MIM; 600103; -;
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0017158; P:regulation of calcium ion dependent exocytosis; ISS.
 CC GO; GO:0016181; P:synaptic vesicle transport; ISS.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR002149; LRI.
 CC InterPro; IPR001565; Synaptotagmin.
 CC Pfam; PF00168; C2; 2.
 CC PRINTS; PR00399; SYNAPTOTAGMIN.
 CC SMART; SM00239; C2; 2.
 CC PROSITE; PS00499; C2_DOMAIN_1; 2.
 CC PROSITE; PS50004; C2_DOMAIN_2; 2.
 CC Transmembrane; Repeat; Synapse.
 CC DOMAIN 1 16 VESICULAR (POTENTIAL).
 CC TRANSMEM 17 37 POTENTIAL.
 CC DOMAIN 38 425 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 147 297 PHOSPHOLIPID BINDING (PROBABLE).
 CC DOMAIN 155 258 C2 DOMAIN 1.
 CC DOMAIN 289 392 C2 DOMAIN 2.
 CC SEQUENCE 425 AA; 47958 MW; DA3D4CB175CB528D CRC64;
 CC
 CC Query Match 100.0%; Score 2201; DB 1; Length 425;
 CC Best Local Similarity 100.0%; Pred. No. 6.4e-145;
 CC Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1 MAPITTSREEDDEIPTVVGIFSAFGLVFTVSLFAMICQRRKSSKNKTPPKYFVHLKGV 60
 CC 1 MAPITTSREEDDEIPTVVGIFSAFGLVFTVSLFAMICQRRKSSKNKTPPKYFVHLKGV 60
 CC 61 DTYPENLNKKKFGADKKNEKNKPAVPKNSIHLDLEKRDNLGNFPKTNLKPSPDLN 120
 CC 61 DTYPENLNKKKFGADKKNEKNKPAVPKNSIHLDLEKRDNLGNFPKTNLKPSPDLN 120
 CC 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTFLFSLNFKFAFVNIKEARGL 180
 CC 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTFLFSLNFKFAFVNIKEARGL 180
 CC 181 PAMDEQSMSTSDPIKMTILPEKKHKVKTIVRLTLPAPDETFTFYGIPYTOIELALHF 240
 CC 181 PAMDEQSMSTSDPIKMTILPEKKHKVKTIVRLTLPAPDETFTFYGIPYTOIELALHF 240
 CC 241 TILSFDRSRDIIIGVLLPLSGIELSEGMLMNRRIKENVRKSSGRGELLISLCYQST 300
 CC 241 TILSFDRSRDIIIGVLLPLSGIELSEGMLMNRRIKENVRKSSGRGELLISLCYQST 300
 CC 301 TNLTLVVLKARHLKPSDVSGLSDPYKVNKLHAKKRIISKKTHVKKCTPNVFNELFVF 360
 CC 301 TNLTLVVLKARHLKPSDVSGLSDPYKVNKLHAKKRIISKKTHVKKCTPNVFNELFVF 360
 CC 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVLAAGAGTGGEHWKEICDYPRQIAKWH 420

Db 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVLAAGAGTGGEHWKEICDYPRQIAKWH 420
 QY 421 VLCDG 425
 Db 421 VLCDG 425

RESULT 2

SYT4_RAT
 ID SYT4_RAT STANDARD; PRT; 425 AA.
 AC P50232;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Synaptotagmin IV (SYTIV).
 GN SYT4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95085772; PubMed=7993622;
 RA Ullrich B., Li C., Zhang J.Z., McMahon H., Anderson R.G., Geppert M.,
 RA Suedhof T.C.;
 RT "Functional properties of multiple synaptotagmins in brain.";
 RL Neuron 13:1281-1291(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9519312; PubMed=7892240;
 RA Vician L., Lim I.K., Ferguson G., Tocco G., Baudry M., Herschman H.R.;
 RT "Synaptotagmin IV is an immediate early gene induced by
 RT depolarization in PC12 cells and in brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2164-2168(1995).
 CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
 CC secretory vesicles through Ca(2+) and phospholipid binding to the
 CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
 CC vesicles.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
 CC
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 CC
 CC EMBL; U14398; AAA68519.1; -;
 CC EMBL; L38247; AAA67327.1; -;
 CC PIR; I59355; I59355.
 CC HSP; P21707; 1BYN.
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0017158; P:regulation of calcium ion dependent exocytosis; ISS.
 CC GO; GO:0016181; P:synaptic vesicle transport; ISS.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR001565; Synaptotagmin.
 CC Pfam; PF00168; C2; 2.
 CC PRINTS; PR00360; C2DOMAIN.
 CC SMART; SM00239; SYNAPTOTAGMIN.
 CC PROSITE; PS00499; C2_DOMAIN_1; 2.
 CC PROSITE; PS50004; C2_DOMAIN_2; 2.
 CC Transmembrane; Repeat; Synapse.
 CC DOMAIN 1 16 VESICULAR (POTENTIAL).
 CC TRANSMEM 17 37 POTENTIAL.
 CC DOMAIN 38 425 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 147 297 PHOSPHOLIPID BINDING (PROBABLE).
 FT DOMAIN 155 258 C2 DOMAIN 1.
 FT DOMAIN 289 392 C2 DOMAIN 2.
 SQ SEQUENCE 425 AA; 47685 MW; 6AC88E00878936BB CRC64;
 Query Match 91.1%; Score 2006; DB 1; Length 425;
 Best Local Similarity 89.9%; Pred. No. 1.9e-131;
 Matches 382; Conservative 21; Mismatches 22; Indels 0; Gaps 0;
 QY 1 MAPITTSREEFDEIPTVVGIISAFGLVFTVSLFAMICCCQKSKSNKTPPYKPVHVLKGV 60
 Db 1 MAPITTSRVEFDEIPTVVGIISAFGLVFTVSLFAMICCCQKSKSNKTPPYKPVHVLKGV 60
 QY 61 DIYPENLNKKFGADDKNEVKNKPAVKNLSHLDEKRDINGNFPKTNLKPSPSDLEN 120
 Db 61 DIYPENLNKKFGADDKNEVKNKPAVKNLSHLDEKRDINGNFPKTNLKPSPSDLEN 120
 QY 121 ATPKLFLEGEKESVPSLSKSTSLTSEKQKGLTFLPSLEYNFERKAFVNNKEARGL 180
 Db 121 VTPKLFETEKESVPSLSKSTSLTSEKQKGLTFLPSLEYNFERKAFVNNKEARGL 180
 QY 181 PAMDEQSMTPDYIKMTILPEKKHKVTRVLRKTLDPVDEFTTFYGVYPYHQLSLHF 240
 Db 181 PAMDEQSMTPDYIKMTILPEKKHKVTRVLRKTLDPVDEFTTFYGVYPYHQLSLHF 240
 QY 241 TILSFDRSDDIIGEVILPLSGIELSGKMLMREIKRNVKSGRGELLISLCYQST 300
 Db 241 TILSFDRSDDIIGEVILPLSGIELSGKMLMREIKRNVKSGRGELLISLCYQST 300
 QY 301 TNLTVVVLKARHLPKSDVSGLSDPYVKNLYHAKRKISKKTHVKKCTPNAVFNELFVF 360
 Db 301 TNLTVVVLKARHLPKSDVSGLSDPYVKNLYHAKRKISKKTHVKKCTPNAVFNELFVF 360
 QY 361 DIPCEGLDISVEFLVLDSESGRNEVIGQLVGLAAEGTGGHWEICDYPFRQIAKWH 420
 Db 361 DIPCEGLDISVEFLVLDSESGRNEVIGQLVGLAAEGTGGHWEICDYPFRQIAKWH 420
 QY 421 VLCDG 425
 Db 421 MLCDG 425
 RESULT 3
 SYTB_MOUSE
 ID SYTB_MOUSE STANDARD; PRT; 425 AA.
 AC P40749;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Synaptotagmin IV (SytIV).
 GN SYT4 OR SYT3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=94336712; PubMed=8058779;
 RA Hilbush B.S., Morgan J.I.;
 RT "A third synaptotagmin gene, Syt3, in the mouse."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:8195-8199(1994).
 CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
 CC secretory vesicles through Ca(2+) and phospholipid binding to the
 CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
 CC vesicles.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY REGIONS OF THE NERVOUS
 CC SYSTEM BUT IS UNDETECTABLE IN EXTRA NEURAL TISSUES.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.

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EMBL; U10355; AAA20971.1; -.
 DR HSSP; P21707; 1BYN.
 DR MGD; MGI:101759; SYC4.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0017158; P:regulation of calcium ion dependent exocytosis; TAS.
 DR GO; GO:0016181; P:synaptic vesicle transport; TAS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002149; LRI.
 DR InterPro; IPR001565; Synaptotagmin.
 DR Pfam; PF00168; C2; 2.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00399; SYNAPTOTAGMN.
 DR SMART; SM00239; C2; 2.
 DR PROSITE; PS00499; C2 DOMAIN 1; 2.
 DR PROSITE; PS50004; C2 DOMAIN 2; 2.
 KW Transmembrane; Repeat; Synapse.
 FT DOMAIN 1 16 VESICULAR (POTENTIAL).
 FT TRANSMEM 17 37 POTENTIAL.
 FT DOMAIN 38 425 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 147 297 PHOSPHOLIPID BINDING (PROBABLE).
 FT DOMAIN 155 258 C2 DOMAIN 1.
 FT DOMAIN 289 392 C2 DOMAIN 2.
 SQ SEQUENCE 425 AA; 47630 MW; D1900D475C163821 CRC64;

Query Match 90.3%; Score 1988; DB 1; Length 425;
 Best Local Similarity 89.4%; Pred. No. 3.3e-130;
 Matches 380; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

QY 1 MAPITTSREEFDEIPTVVGIISAFGLVFTVSLFAMICCCQKSKSNKTPPYKPVHVLKGV 60
 Db 1 MAPITTSRVEFDEIPTVVGIISAFGLVFTVSLFAMICCCQKSKSNKTPPYKPVHVLKGV 60
 QY 61 DIYPENLNKKFGADDKNEVKNKPAVKNLSHLDEKRDINGNFPKTNLKPSPSDLEN 120
 Db 61 DIYPENLNKKFGADDKNEVKNKPAVKNLSHLDEKRDINGNFPKTNLKPSPSDLEN 120
 QY 121 ATPKLFLEGEKESVPSLSKSTSLTSEKQKGLTFLPSLEYNFERKAFVNNKEARGL 180
 Db 121 VTPKLFETEKESVPSLSKSTSLTSEKQKGLTFLPSLEYNFERKAFVNNKEARGL 180
 QY 181 PAMDEQSMTPDYIKMTILPEKKHKVTRVLRKTLDPVDEFTTFYGVYPYHQLSLHF 240
 Db 181 PAMDEQSMTPDYIKMTILPEKKHKVTRVLRKTLDPVDEFTTFYGVYPYHQLSLHF 240
 QY 241 TILSFDRSDDIIGEVILPLSGIELSGKMLMREIKRNVKSGRGELLISLCYQST 300
 Db 241 TILSFDRSDDIIGEVILPLSGIELSGKMLMREIKRNVKSGRGELLISLCYQST 300
 QY 301 TNLTVVVLKARHLPKSDVSGLSDPYVKNLYHAKRKISKKTHVKKCTPNAVFNELFVF 360
 Db 301 TNLTVVVLKARHLPKSDVSGLSDPYVKNLYHAKRKISKKTHVKKCTPNAVFNELFVF 360
 QY 361 DIPCEGLDISVEFLVLDSESGRNEVIGQLVGLAAEGTGGHWEICDYPFRQIAKWH 420
 Db 361 DIPCEGLDISVEFLVLDSESGRNEVIGQLVGLAAEGTGGHWEICDYPFRQIAKWH 420
 QY 421 VLCDG 425
 Db 421 MLCDG 425

RESULT 4
 SYTB_MOUSE
 ID SYTB_MOUSE STANDARD; PRT; 430 AA.
 AC Q9R0N3;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Synaptotagmin XI (SytXI).
 GN SYT11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Cerebellum;
 RX MEDLINE=20002669; PubMed=10531343;
 RA Fukuda M., Kanno E., Mikoshiba K.;
 RT "Conserved N-terminal cysteine motif is essential for homo- and
 RT heterodimer formation of synaptotagmins III, V, VI, and X.";
 RL J. Biol. Chem. 274:31421-31427(1999).
 CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
 CC secretory vesicles through Ca(2+)-dependent exocytosis of
 CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis (By similarity).
 CC -!- SUBUNIT: Homodimer. Can also form heterodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
 CC VESICLES (By similarity).
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
 CC
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 CC
 CC -----
 CC EMBL: AB026808; BAA85780.1; --
 CC HSSP: P21707; IRSY.
 CC MGD: MGI:185947; Syt11.
 CC GO: GO:0005887; C:integral to plasma membrane; IDA.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002149; LRI.
 CC InterPro: IPR001565; Synaptotagmin.
 CC Pfam: PF00168; C2; 2.
 CC PRINTS: PR00399; SYNAPTOTAGMIN.
 CC SMART: SM00239; C2; 2.
 CC PROSITE: PS00499; C2 DOMAIN 1; FALSE_NEG.
 CC PROSITE: PS50004; C2 DOMAIN 2; 2.
 CC Transmembrane; Repeat; Synapse.
 CC DOMAIN 1 15 VESICULAR (POTENTIAL).
 CC TRANSMEM 16 36 POTENTIAL.
 CC DOMAIN 37 430 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 173 261 C2 DOMAIN 1.
 CC DOMAIN 303 396 C2 DOMAIN 2.
 CC SEQUENCE 430 AA; 48359 MW; 25E7CDFC4B4BE036 CRC64;
 Query Match 53.0%; Score 1167.5; DB 1; Length 430;
 Best Local Similarity 51.0%; Pred. No. 1.7e-73;
 Matches 233; Conservative 70; Mismatches 93; Indels 61; Gaps 8;
 QY 1 MAPITTSREDFEIPVVGIFSAFLGVFTVS--LFAWICQKSSKSNKTPPYKFFVHLK 58
 DB 1 MAEITNRPSPDVSFVAAGLIGASLVVCSVTVFVWTCCHQAEKHKTPPYKFFIHLK 60
 QY 59 GVDIYIPENLNSKKK-----FGADDKNEVKNKPAVPKNS 91
 DB 61 GISYIPETLSNKKIKVRRDKDPPRESGRGNLLINAEGLLSHDKDPRGSPSPSCMDQ 120
 QY 92 LHLDLKSLDNGNF--PKTNLRGSPDLNATPKLFLEGEKESVSPESLKSSTLSLTSSE 149
 DB 121 LPI-----KRDYGBELSPMTSLTP-----GESKPTSP-----SSPE 152
 QY 150 KOEKLGLTFFSLYENFERKAFVNVNIKEARGLPAMDQSMTSDFYIKWTLPEKKHKVYKTR 209

Db 153 EDVNLGSLTFSVDYVNFPAKALVVTIQEAHGLPVMDDQTOGSDPYIKMTILPKRHRVYKTR 212
 QY 210 VLKRTLPADFETFTFYGIPYQIQELAHFTILSFDRSDDIIGEVILPLSGIELSEG 269
 Db 213 VLKRTLPADFETFTFYGIPYQIQELAHFTILSFDRSDDIIGEVILPLSGIELSEG 272
 QY 270 KMLMREIIRKRVKSGRGELLISLCYQSTNTTLTVVVLKARHLPSKDVSGLS-DFYVK 328
 Db 273 KVQLTRDIIRKRIKQICSRGELQVSLSYQVAQRMTVVVVKARHLPKMDITGLSGNPFYK 332
 QY 329 VNLVYHAKKRISKKTHVKKCTPNAFVNFELFVDPICBGLIEDISVFLVLDSEGRSNEVI 388
 Db 333 VNYVYGRKRIAKKTHVKKCTPNAFVNFELFVDPICBGLIEDISVFLVLDSEGRSNEVI 392
 QY 389 GOLVLGAAAEAGT-GGEHWKEICDYPRIQIAKHWLVD 424
 Db 393 GRLLIGHSVTTSAGAEHWREVCESPRKPIAKHWLSE 429
 RESULT 5
 SYTB HUMAN STANDARD; PRT; 431 AA.
 AC Q9BT88;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Synaptotagmin XI (SytXI).
 GN SYT11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isozaki T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
 CC secretory vesicles through Ca(2+) and phospholipid binding to the
 CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis (By similarity).
 CC -!- SUBUNIT: Homodimer. Can also form heterodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
 CC VESICLES (By similarity).
 CC -!- SIMILARITY: Contains 2 C2 domains.

```

CC -1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AK074931; BAC11300.1; -
CC EMBL; BC004291; AAH04291.1; -
CC EMBL; BC013690; AAH13690.1; -
CC HSSP; P21707; IRSY.
CC Genew; HGNC:19239; SYTL1.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002149; LRI.
CC InterPro; IPR001565; Synaptotagmin.
CC Pfam; PF00168; C2; 2.
CC PRINTS; SM00239; C2; 2.
CC SMART; SM00239; C2; 2.
CC PROSITE; PS00499; C2_DOMAIN 1; FALSE_NEG.
CC PROSITE; PS00004; C2_DOMAIN 2; 2.
CC TRANSMEMBRANE; Repeat; Synapse.
CC DOMAIN 1 15 VESICULAR (POTENTIAL).
CC TRANSMEM 16 36 POTENTIAL.
CC DOMAIN 37 431 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 174 262 C2_DOMAIN 1.
CC DOMAIN 304 397 C2_DOMAIN 2.
CC SEQUENCE 431 AA; 48306 MW; A7F76AD745COFF7D CRC64;

Query Match 52.8%; Score 1162; DB 1; Length 431;
Best Local Similarity 52.4%; Pred. No. 4e-73;
Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;

QY 1 MAPITTSREDFEIPVTVGIFSAFLVFTVS--LPFWTCCORRKSNSKNTPPYKPVHLK 58
Db 1 MAEITNIRPSFDVSPVAAGLIGASVLVVCVSVTVFVMSCHQQAQKHKNPYKFIHMLK 60

QY 59 GVDIYPENLNSKKKFGADDKNEVKNKPAVKPNSLHLDLEK-----RLNGNFP----- 113
Db 61 GSIVPETLSNKKELIKVRDKDQSGHRESGRNLLVNAESGLLSHDDPRGSPASCIQ 114

QY 114 SPSDLENATPKL-----FLEGEKESVSPESLSKSTSLTSEEKQELGTLFFSLVYNFERKA 169
Db 115 SGSCIDQLPKMDYGEELRSPITSLTGESK-TTSPSPSEEDVMLGSLTFVSDVYNFERKA 173

QY 170 FVYNKEARGLPAMDQSGTSDPYIKMTILPEKKHKVTRVLRKTLDPAPDETFTFYGIP 229
Db 174 LVVTIQEAHGLPVMDQSGTSDPYIKMTILPEKKHKVTRVLRKTLDPVDEFTFYGIP 233

QY 230 YTGIOELALHFTLSDFRSDDIIGVLIPLSGIELSEGKMLNRETIKRNVRKSGRG 289
Db 234 YSQQLVHLVLFSLDFRSDDIIGVLMVPLAGVDFSTGKVTLDIKENIKQICISRG 293

QY 290 ELLISLCYQSTNTLVVVLKARHLPKSDVSGLS-DPAVKVNLVHAKRISKKTHVKK 348
Db 294 ELQVLSYQPVAGMTVVLKARHLPKDDITGLSGNPNVKNVYGRKRIAKKTHVKK 353

QY 349 TPNAVNELFVDFIPCEGLEDDISVEFLVLDSEGRSNEVIGQLVGA-AAAGTGGEHWKE 407
Db 354 TLNPIFNESFIYDPTDLLDISIEFLVIDFRTKNEVGRLLILGAHSVTSAGAEHWRE 413

QY 408 ICYPRQAKHVLCD 424
Db 414 VCESPRKPVAKHSLSE 430

RESULT 6
SYTB RAT
ID SYTB RAT
AC O08835;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Synaptotagmin XI (SYTXI).
GN SYTL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97306341; PubMed=9162066;
RA von Poser C., Ichtchenko K., Shao X., Rizo J., Suedhof T.C.;
RT "The evolutionary pressure to inactivate. A subclass of synaptotagmins
RL J. Biol. Chem. 272:14314-14319(1997).
CC -1- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
CC secretory vesicles through Ca(2+)- and phospholipid binding to the
CC C2 domain or may serve as Ca(2+) sensors in the process of
CC vesicular trafficking and exocytosis (By similarity).
CC -1- SUBUNIT: Homodimer. Can also form heterodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
CC VESICLES (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in brain and at lower levels
CC in other tissues.
CC -1- SIMILARITY: Contains 2 C2 domains.
CC -1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF000423; AAB58344.1; -
CC HSSP; P21707; IRSY.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002149; LRI.
CC InterPro; IPR001565; Synaptotagmin.
CC Pfam; PF00168; C2; 2.
CC PRINTS; PR00399; SYNAPTOTAGMIN.
CC SMART; SM00239; C2; 2.
CC PROSITE; PS00499; C2_DOMAIN 1; FALSE_NEG.
CC PROSITE; PS00004; C2_DOMAIN 2; 2.
CC TRANSMEMBRANE; Repeat; Synapse.
CC DOMAIN 1 15 VESICULAR (POTENTIAL).
CC TRANSMEM 16 36 POTENTIAL.
CC DOMAIN 37 430 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 158 261 C2_DOMAIN 1.
CC DOMAIN 292 396 C2_DOMAIN 2.
CC SEQUENCE 430 AA; 48268 MW; C1FA13CB9177C825 CRC64;

Query Match 52.5%; Score 1156.5; DB 1; Length 430;
Best Local Similarity 51.5%; Pred. No. 9.6e-73;
Matches 228; Conservative 78; Mismatches 104; Indels 33; Gaps 7;

QY 1 MAPITTSREDFEIPVTVGIFSAFLVFTVS--LPFWTCCORRKSNSKNTPPYKPVHLK 58
Db 1 MAEITNIRPSFDVSPVAAGLIGASVLVVCVSVTVFVMTCCHQQAQKHKTPPYKFIHMLK 60

QY 59 GVDIYPENLNSKKKFGADDKNEVKNKPAVKPNSLHLDLEK-----RLNGNFP----- 106
Db 61 GSIVPETLSNKKELIKVRDKDQSGHRESGRNLLVNAESGLLSHDDPRGSPASCIQ 120

QY 107 ---KTNLKPSPSDLENATPKLFLGEKESVSPESLSKSTSLTSEEKQELGTLFFSLFY 163
Db 121 LPIKRDYGEELRSPMTSLT-----GSKTSP-----SSPEEDVMLGSLTFVDY 166

QY 164 NPERKAFVYNKEARGLPAMDQSGTSDPYIKMTILPEKKHKVTRVLRKTLDPAPDETFT 223
Db 167 NFPKALVVTIQEAHGLPVMDQSGTSDPYIKMTILPEKKHKVTRVLRKTLDPVDEFT 226

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Qy	224	TFYGIPTQIQELALHFTLGFDRSRDIIIGEVLPISGILSGSLGKMLMREIITKNRV	283
Db	227	TFYGIPTQIQELALHFTLGFDRSRDIIIGEVLPISGILSGSLGKMLMREIITKNRV	286
Qy	284	KSSRGELLISLCYQSTNTLTVVVLKARHLPKSDVSGLS-DPYKVNLIYHAKGISKKK	342
Db	287	KCISRGELQVLSLQVPAQRMTVVVLKARHLPFQMDITGLSGNPYKVNLYYGRKIAKKK	346
Qy	343	THVKKCTPNVAFNELFDPIDICEGLDTSVFLVDLSDSGSNSEVIGOLVGLAAAGT-G	401
Db	347	THVKKCTLPINFESFYDITDLDLPDISLBEFLVDFTTKNEVVGRLILGAHSTTSG	406
Qy	402	GEHWKGTCDYPRQIAKWHVLCD	424
Db	407	AEHWRVCESPKPKVAKWHSLS	429

RESULT 7

SYT7_MOUSE		
ID	SYT7_MOUSE	STANDARD; PRT; 403 AA.
AC	Q9R0N7;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Synaptotagmin VII (SyTVII).	
GN	SYT7.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TaxID	10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ICK; TISSUE=Cerebellum;	
RC	MEDLINE=20002669; PubMed=10531343;	
RA	Fukuda M., Kanno E., Mikoshiba K.;	
RT	"Conserved N-terminal cysteine motif is essential for homo- and heterodimer formation of synaptotagmins III, V, VI, and X.";	
RL	J. Biol. Chem. 274:31421-31427(1999).	
CC	-!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of secretory vesicles through Ca(2+) and phospholipid binding to the C2 domain or may serve as Ca(2+) sensors in the process of vesicular trafficking and exocytosis (By similarity).	
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC VESICLES (By similarity).	
CC	-!- SIMILARITY: Contains 2 C2 domains.	
CC	-!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.	

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CC entities requires a license agreement (See <http://www.ebi.ac.uk/ebis/sib.ch/announcement/>
CC or send an email to license@ebi-sib.ch).

CC	EMBL; AB026804; BAA85776.1; -.
CC	HSSP; P21707; IRSY.
DR	MGI; MGI:1859545; Syt7.
DR	InterPro; IPR000008; C2.
DR	InterPro; IPR002149; LRI.
DR	InterPro; IPR001565; Synaptotagmin.
DR	Fram; FR00168; C2; 2.
DR	PRINTS; PR00360; C2DOMAIN.
DR	PRINTS; PR00399; SYNAPTOTAGMN.
DR	PROSITE; PS00499; C2_DOMAIN_1; 2.
DR	PROSITE; PS50004; C2_DOMAIN_2; 2.
KW	Transmembrane; Repeat; Synapse.
FT	DOMAIN 1 16 VESICULAR (POTENTIAL).
FT	TRANSMEM 17 37 POTENTIAL.
FT	DOMAIN 38 403 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 137 239 C2 DOMAIN 1.
FT	DOMAIN 268 371 C2 DOMAIN 2.

[illegible]

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RESULT 8
SY65_DROME STANDARD; PRT; 474 AA.
ID SY65_DROME STANDARD; PRT; 474 AA.
P21521;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Synaptotagmin (p65).
SYT.
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=91093190; PubMed=1840599;
RX Perin M.S., Johnston P.A., Oezcelik T., Jahn R., Francke U.,
RA Suedhof T.C.;
RA "Structural and functional conservation of synaptotagmin (p65) in
RT Drosophila and humans."
RT J. Biol. Chem. 266:615-622(1991).
CC -!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
CC BACKBONE.
CC -!- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
CC -!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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RESULT 12
SYT2 RAT


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RX MEDLINE=93313960; PubMed=8391930;
RA Nonet M.L., Grundahl K., Meyer B.J., Rand J.B.;
RT "Synaptic function is impaired but not eliminated in C. elegans
RL mutants lacking synaptotagmin.";
RN Cell 73:1291-1305(1993).
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RL Du Z.;
RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
CC BACKBONE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND VESICLE-LIKE
CC STRUCTURES.
CC -!- TISSUE SPECIFICITY: LOCALIZED TO REGIONS KNOWN TO BE RICH IN
CC SYNAPSES AND APPEARS TO BE ASSOCIATED WITH SYNAPTIC VESICLES.
CC ALSO FOUND IN SOME NONNEURONAL SECRETORY STRUCTURES.
CC -!- DISEASE: MUTANTS EXHIBIT SEVERE BEHAVIORAL ABNORMALITIES THAT ARE
CC CHARACTERISTIC OF DEFICIENCIES IN SYNAPTIC FUNCTION, INCLUDING
CC SEVERE LOCOMOTION, FEEDING, AND DEPECATION DEFECTS.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L15302; AAA28145.1; -;
CC EMBL; U55856; AAA98023.1; -;
CC PIR; A40707; A40707.
CC HSP; P21707; IRSY.
CC WormPep; F31E8.2; CE02711.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002149; LRI.
CC InterPro; IPR001565; Synaptotagmin.
CC Pfam; PF00168; C2; 2.
CC PRINTS; PR00360; C2DOMAIN.
CC PRINTS; PR00399; SYNAPTOTAGMN.
CC SMART; SM00239; C2; 2.
CC PROSITE; PS00499; C2_DOMAIN_1; 2.
CC PROSITE; PS50004; C2_DOMAIN_2; 2.
CC Transmembrane; Repeat; Synapse; Glycoprotein.
KW DOMAIN 1 69 VESICULAR (POTENTIAL).
FT TRANSMEM 70 96 POTENTIAL.
FT DOMAIN 97 441 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 175 262 C2 DOMAIN 1.
FT DOMAIN 306 397 C2 DOMAIN 2.
SQ SEQUENCE 441 AA; 49904 MW; F8D174337EB472DB CRC64;

Query Match 27.0%; Score 594; DB 1; Length 441;
Best Local Similarity 40.2%; Pred. No. 7.2e-34;
Matches 148; Conservative 57; Mismatches 111; Indels 52; Gaps 14;

QY 70 KKFEGADDKNEVKNKPAVPKNSLHLDLEKRDINGNPK-----TWLKPSPSDLENAT 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
97 RKLFGKXHGK-KNK-----KGLKGFPGKGDVVDGKNIQ-GMAQDLELG 141

QY 123 PKLFLGEKESVPSLSKSTSLTSEKQE-KLGTLFFSLVYNFERKAFVVIKEAGLP 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
142 DAM-EQNEKEQ-----AAEEVKLGRIOYKLDYDFQQQLIVTVIQAEPL 187

QY 182 AMEQSMTSDPYIKMTILPEKKHKVRYLRKTLDPAFDEFTTFYIGIPYQIQELALHFT 241
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
188 GMD-MSGTSDPYKLYLLPEKKKKVETKVRKTLNPFVETFLP-KVAFNEITAKTILVFA 245

QY 242 ILSFDRSRDDIIIEVLPISGIEHSEGHMLMNRRI-----KRNVRKSSRGELLISLC 296

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Db	246	IYDFRSKHQD	IGOVLIPLGKIDL	--GAVIEEWKDIAPPDDKEAEKS--	LGDI	CFSLR	301
Qy	297	YQSTNTNT	TVVVLKARHL	PKSDVGLSDPYVKVNL	YHAKKRISKKTHVKKCTPNAVNE		356
Db	302	YVPTAGKLT	VVILEAKNL	KQMDVGLSDPYVKIV	LMQGGKRLKKKTSIKKCTLNPYNE		361
Qy	357	LFVFDIPCEGL	EDISVFLVD	SERGSNEVIGQVLGAA	AEGTGGE--HWKEICDYPRR		414
Db	362	SFSEVPFEQI	KVQKVSIL	MTVMDYKLSG	DAIGRCILG--CNGTGAELRHWM	MLASPRR	419
Qy	415	QIAKWHVL	422				
Db	420	PIAQWHTL	427				
RESULT 15							
ID	SYTA	RAT	STANDARD;	PRT;	498	AA.	
AC	O08625;						
DT	16-OCT-2001	(Rel. 40, Created)					
DT	16-OCT-2001	(Rel. 40, Last sequence update)					
DT	28-FEB-2003	(Rel. 41, Last annotation update)					
DE	Synaptotagmin X (SytX)	(Fragment).					
GN	Syt10.						
OS	Rattus norvegicus (Rat).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
NCBI	TaxID=10116;						
RN	[1]						
FP	SEQUENCE FROM N.A.						
RC	STRAIN=Sprague-Dawley;						
RX	MEDLINE=97226006; PubMed=9122248;						
RA	Babity J.M., Armstrong J.N., Plumier J.C., Currie R.W.,						
RA	Robertson H.A.;						
RT	"A novel seizure-induced synaptotagmin gene identified by differential						
RT	display."						
RL	Proc. Natl. Acad. Sci. U.S.A. 94:2638-2641(1997).						
CC	-[- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of						
CC	secretory vesicles through Ca(2+) and phospholipid binding to the						
CC	C2 domain or may serve as Ca(2+) sensors in the process of						
CC	vesicular trafficking and exocytosis (By similarity).						
CC	-[- SUBUNIT: Homodimer. Can also form heterodimer (By similarity).						
CC	-[- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC						
CC	VESICLES (By similarity).						
CC	-[- SIMILARITY: Contains 2 C2 domains.						
CC	-[- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.						
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation						
CC	at the European Bioinformatics Institute. There are no restrictions on its						
CC	use by non-profit institutions as long as its content is in no way						
CC	modified and this statement is not removed. Usage by and for commercial						
CC	entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).						
CC	EMBL; U85513; AAB51686.1; --						
DR	PIR; PC6300; PC6300.						
DR	HSP; P21707; IBYN.						
DR	InterPro; IPR000008; C2.						
DR	InterPro; IPR002149; LRI.						
DR	InterPro; IPR001565; Synaptotagmin.						
DR	Pfam; PF00168; C2; 2						
DR	PRINTS; PR00360; C2DOMAIN.						
DR	PRINTS; PR00399; SYNAPTOTAGMN.						
DR	SMART; SM00239; C2; 2.						
DR	PROSITE; PS00499; C2 DOMAIN 1; 2.						
DR	PROSITE; PS00004; C2 DOMAIN 2; 2.						
DR	Transmembrane; Repeat; Synapse.						
FT	DOMAIN 1 55						
FT	FT	VESICULAR (POTENTIAL).					
FT	TRANSMEM 56 76						
FT	DOMAIN 77 >498						
FT	DOMAIN 233 334						
FT	DOMAIN	C2 DOMAIN 1					

```
FT DOMAIN 365 468 C2 DOMAIN 2.
FT NON_TER 498
SQ SEQUENCE 498 AA; 56411 MW; 620BD7CD372057DE CRC64;

Query Match      26.9%; Score 592; DB 1; Length 498;
Best Local Similarity 34.6%; Pred. No. 1.2e-33;
Matches 158; Conservative 72; Mismatches 156; Indels 70; Gaps 16;

QY 20 IFSAFGL-VFTVSLFA-WICQKSKSKNKTTPPKVHVHLKGVDIYPENLNS--KKKGA 75
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 DDKNEV-KKPAVPKNSLHLDLKRDLNGNFP---KTNLK-----PGSPS 116
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 EEKEVEENEKEPAK-AIEPAIKISHTSPDIPAEVQTALKEHLKHARVQQTDTPTSS 169
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 -----DLENATPKLFLGKES-----VSPESLKSSTLTSE-----EK 150
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 170 RHNSFRHLPRQNVSSVDFSMGTPEVLQGETRTSIGR.KPELYKQK-SVDSEGNKDD 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 151 QEKLGLTFLFSLEYNFERKAFVNNIKKARGHPAMDEQSWTSDPYIKMTILPEKKHKVTRV 210
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 VKTCGLNFALQDYENELLVVKIINKALDPAKOSTG-TSDPYVKIYLLPDRKKKQTRV 287
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 LRKTLDPADFETTFYGIPTQIQELALHFTILSDFRSGRDDIIGEVLIPLSGIELSEK 270
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 HRKTLNPLFDELQF-PVYDQLSNRKLHFSYDFDRFRSHDMIGEVLID-----NLFEVS 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 MIMREIIRNVR-----KSSRGCELLISLCYOSTTNTLTVVVLKARHLPKSDVSLSDPY 326
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 343 DLSREATVWKDIHCATTESMDLGEIMFSLCYLPTAGRMWLTWIKCRNLKAMDITGSSDPY 402
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 VKVNLVHAKKRIKKKTHVKKTPNAVFNELFVFDIPCGLIEDISVEFLVLDSEGRSNE 386
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 403 VKVSLMCEGRLLKKRKTTKNTLNPVYNEALIFDIPPENVDQVSLCIAVMDYDRVGHNE 462
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 387 VIGQLVLGAAAGTGGEHMKICDYPKQIAKWHVL 422
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 463 VIGVCRIGLDAEGLGRDHWNEMLAYHRKEPITHHPL 498
```

Search completed: February 20, 2004, 13:13:18
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 13:10:35 ; Search time 39 Seconds

(without alignments)
2812.112 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREEFDEIPTVVGI.....KEICDYPRQIAKHWLVDG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_arChaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_arChaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1999	90.8	425	11	Q8BGH3
2	1994	90.6	425	11	Q8BRL6
3	1160.5	52.7	430	11	Q925B6
4	1159	52.7	431	4	Q96SU2
5	1153	52.4	431	4	Q8IXU3
6	874	39.7	245	11	Q8QZS8
7	759	34.5	474	5	Q8SYD5
8	757	34.4	474	5	Q9UGP7
9	645.5	29.3	357	5	Q9GRB0
10	627.5	28.5	403	11	Q62747
11	627	28.5	424	5	Q25393
12	622.5	28.3	474	5	Q9VVG7
13	621.5	28.2	447	11	Q8CF96
14	621	28.2	403	5	Q07529
15	617.5	28.1	472	5	Q9VVG8
16	615.5	28.0	518	11	Q8CF95

ALIGNMENTS

RESULT 1

Q8BGH3 Q8BGH3 PRELIMINARY; PRT; 425 AA.
AC Q8BGH3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Synaptotagmin 4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Dorsal root ganglion, Medulla oblongata, and Pancreas;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK032106; BAC27705.1; -
DR EMBL; AK050515; BAC34301.1; -
DR EMBL; AK083960; BAC39080.1; -
SQ SEQUENCE 425 AA; 47659 MW; 9A01144898CDFCEB CRC64;

Query Match

Best Local Similarity 90.8%; Score 1999; DB 11; Length 425;
Matches 382; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 1 MAPITTSREEFDEIPTVVGIFSAFLVFTVSLFAWICCOCKSSKSNKTPPYKFFVHLKGV 60

Db 1 MAPITTSREEFDEIPTVVGIFSAFLVFTVSLFAWICCOCKSSKSNKTPPYKFFVHLKGV 60

QY 61 DYIPENLNKKFGADDKNEVKKNKPAVPKNSLHLDLEKRLDNGNFPKTNLKPSPDLN 120

Db 61 DYIPENLNKKFGADDKNEVKKNKPAVPKNSLHLDLEKRLDNGNFPKTNLKPSPDLN 120

Q99P37 rattus norv
Q99P36 rattus norv
Q99P35 rattus norv
Q99P34 rattus norv
Q99P33 rattus norv
Q99P38 rattus norv
Q99P33 rattus norv
Q8bmf3 manduca sex
Q8bmf5 homo sapien
Q8r0el mus musculu
Q62746 rattus norv
Q8n9i0 homo sapien
Q9qk7 mus musculu
Q9r0n8 mus musculu
Q8c86 mus musculu
Q925B8 rattus norv
Q9u8r6 dugesia jap
Q95qh7 caenorhabdi
Q925C0 rattus norv
Q9r0n9 mus musculu
Q8c280 mus musculu
Q62748 rattus norv
P91493 caenorhabdi
Q8n640 homo sapien
Q8n521 homo sapien
Q925B7 rattus norv
Q920m7 mus musculu
Q62807 rattus norv
Q9bsw7 homo sapien
Q9nzi8 homo sapien

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QY 121 ATPKFLBGEKESVSPESLSKSTSLTSEEKQKLGTLFFSLEYNFERKAFVNNIKEARGL 180
Db 121 VTPKLFTEKEANSPELSKSTSLTSEEKQKLGTLFFSLEYNFERKAFVNNIKEARGL 180
QY 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPADFETFTFYGIPTQIOELALHF 240
Db 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPADFETFTFYGIPTQIOELALHF 240
QY 241 TILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMNRREIKENVRKSSGRGELLISLCYQST 300
Db 241 TVLSFDRFSDDDIIGEVLIPLSGIELSDGKMLMNRREIKENVRKSSGRGELLISLCYQST 300
QY 301 TMTLTVVVLKARHLPKSDVSGLSLSDPYVKNLYHAKKRISKKKTHVKKCTPNVAFNELFVF 360
Db 301 TMTLTVVVLKARHLPKSDVSGLSLSDPYVKNLYHAKKRISKKKTHVKKCTPNVAFNELFVF 360
QY 361 DIPCEGLIEDISVEFLVLDSEGRSRNEVIGOLVIGAAAGTGGEHWEICDYPFRQIAKWH 420
Db 361 DIPCESLEISVEFLVLDSEGRSRNEVIGRLVIGATAEGSGGHHWEICDYPFRQIAKWH 420
QY 421 VLCDG 425
Db 421 MLC DG 425

RESULT 2
Q8BRL6 PRELIMINARY; PRT; 425 AA.
AC Q8BRL6
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Synaptotagmin 4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK043985; BAC31726.1; --
SQ SEQUENCE 425 AA; 47658 MW; 60011E4F23A7F6EC CRC64;

Query Match 90.6%; Score 1994; DB 11; Length 425;
Best Local Similarity 89.6%; Pred. No. 2.2e-138;
Matches 381; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVS--LFAWICCCQKSSKSNKTPPYKFFVHLKGV 60
Db 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVS--LFAWICCCQKSSKSNKTPPYKFFVHLKGV 60
QY 61 DIYPENLNSKKKFGADDDKNEVKNKPAVPKNSLHLDLEKRDNGNPPKTNLKGPSDLEN 120
Db 61 DIYPENLNSKKKFGADDDKNEVKNKPAVPKNSLHLDLEKRDNGNPPKTNLKGPSDLEN 120
QY 121 ATPKFLBGEKESVSPESLSKSTSLTSEEKQKLGTLFFSLEYNFERKAFVNNIKEARGL 180
Db 121 VTPKLFTEKEANSPELSKSTSLTSEEKQKLGTLFFSLEYNFERKAFVNNIKEARGL 180
QY 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPADFETFTFYGIPTQIOELALHF 240
Db 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPADFETFTFYGIPTQIOELALHF 240
QY 241 TILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMNRREIKENVRKSSGRGELLISLCYQST 300
Db 241 TVLSFDRFSDDDIIGEVLIPLSGIELSDGKMLMNRREIKENVRKSSGRGELLISLCYQST 300

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QY 301 TMTLTVVVLKARHLPKSDVSGLSLSDPYVKNLYHAKKRISKKKTHVKKCTPNVAFNELFVF 360
Db 301 TMTLTVVVLKARHLPKSDVSGLSLSDPYVKNLYHAKKRISKKKTHVKKCTPNVAFNELFVF 360
QY 361 DIPCEGLIEDISVEFLVLDSEGRSRNEVIGOLVIGAAAGTGGEHWEICDYPFRQIAKWH 420
Db 361 DIPCESLEISVEFLVLDSEGRSRNEVIGRLVIGATAEGSGGHHWEICDYPFRQIAKWH 420
QY 421 VLCDG 425
Db 421 MLC DG 425

RESULT 3
Q925B6 PRELIMINARY; PRT; 430 AA.
AC Q925B6
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Synaptotagmin 11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97306341; PubMed=9162066;
RA von Poser C., Ichtchenko K., Shao X., Rizo J., Sudhof T.C.;
RT "The evolutionary pressure to inactivate. A subclass of synaptotagmins
RT with an amino acid substitution that abolishes Ca2+ binding.";
RL J. Biol. Chem. 272:14314-14319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Shin O.-H., von Poser C., Ichtchenko K., Shao X., Rizo J.,
RA Sudhof T.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL; AF375465; AAK56960.1; --
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR Pfam; PF00169; C2; 2.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS00004; C2 DOMAIN 2; 2.
SQ SEQUENCE 430 AA; 48267 MW; FEBE06702BAC2AFB CRC64;

Query Match 52.7%; Score 1160.5; DB 11; Length 430;
Best Local Similarity 51.7%; Pred. No. 3.7e-77;
Matches 229; Conservative 77; Mismatches 104; Indels 33; Gaps 7;

QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVS--LFAWICCCQKSSKSNKTPPYKFFVHLK 58
Db 1 MAEITNTRPSFDVSPFAAGLIGASVIVCVSVTFVFWTCCHQQAEEKKHTPPYKFIHMLK 60
QY 59 GVDIYPENLNSKKKFGADDDKNEVKNKPAVPKNSLHLDLEK-----RDNGNPP----- 106
Db 61 GISIYPTLNKKKILIKVRDDKSHRESGRLNVAESGLLSHDDPRGSPASCIQ 120
QY 107 ---KTNLKPSPSDLENATPKLFLGEEKESVSPESLSKSTSLTSEEKQKLGTLFFSLEY 163
Db 121 LPKRDYGEELRSPMTSLTP-----GSKPTSP-----SSPEEDVMGLSFTSVDY 166
QY 164 NFERKAFVNNIKEARGLPAWDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPADFET 223
Db 167 NFEKALVVTIQEAHGLPVMGQGTQSGSDPYIKMTILPKRHEVTRVLRKTLDPVDETF 226
QY 224 TFGYGIPTQIOELALHFTILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMNRREIKRNV 283
Db 227 TFGYGIPTQIOELALHFTILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMNRREIKRNV 286
QY 284 KSSGRGELLISLCYQSTNTLTVVVLKARHLPKSDVSGLS--DPYKVNLYHAKKRISKKK 342
Db 287 KCLSRGELQVSYSQPVQAQMTVVVLKARHLPKMDITGLSGNPYKVNLYHAKKRISKKK 346

```


DE Similar to synaptotagmin IV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL; BC025207; AAH25207.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR Pfam; PF00168; C2; 2.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS50004; C2 DOMAIN 2; 2.
SQ SEQUENCE 245 AA; 28092 MW; 65B2BFD155D5865F CRC64;

Query Match 39.7%; Score 874; DB 11; Length 245;
Best Local Similarity 65.2%; Pred. No. 2e-56;
Matches 159; Conservative 46; Mismatches 37; Indels 2; Gaps 2;

QY 183 MDSQMTSDPIKMTILPEKKHVKTRVLRKTLDPAFDETFYGIPTQIQELALHFTI 242
DB 1 MDDQTQSGDPVIMKMTILPEKKHVKTRVLRKTLDPVDFETFYGIPTQIQELALHFTI 60
QY 243 LSFDRFRDIIIGHVLPLSGIEISEGKMLMNRRIIKRNVKSSGRGELLISLCYQSTTN 302
DB 61 LSFDRFRDIIIGHVLPLSGIEISEGKMLMNRRIIKRNVKSSGRGELLISLCYQSTTN 302
QY 303 TLTAVVLKARHLPKSDVSGLS-DSYVKNVLYHAKRKISKKTHVKKCTPNAFVNFVFD 120
DB 121 RMVVVLKARHLPKSDVSGLS-DSYVKNVLYHAKRKISKKTHVKKCTPNAFVNFVFD 180
QY 362 IPCEGLEDISVEFVLDSERGSNEVIGQLVGLAAEGT-GGEHWEKICDYPRIAKWH 420
DB 181 IPTDLLPDISIEFLVIDFDRTKNEVVRILGHSHSVTTSAGHWEVREVCSPRPPIAKWH 240
QY 421 VLCD 424
DB 241 SLSE 244

RESULT 7
Q8SYDS PRELIMINARY; PRT; 474 AA.
ID Q8SYDS;
AC Q8SYDS;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 21, Last annotation update)
DE R66711lp.
GN SYTIV OR CG10047.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Berkeley;
RC Scapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL; AY071620; AAL49242.1; -.
DR FlyBase; FBgn028400; SYTIV.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR Pfam; PF00168; C2; 2.

DE SMART; SM00239; C2; 2.
DR PROSITE; PS50049; C2 DOMAIN 1; 1.
DR PROSITE; PS50004; C2 DOMAIN 2; 2.
SQ SEQUENCE 474 AA; 52217 MW; 83853BF326622044 CRC64;

Query Match 34.5%; Score 759; DB 5; Length 474;
Best Local Similarity 38.2%; Pred. No. 1.3e-47;
Matches 179; Conservative 82; Mismatches 137; Indels 70; Gaps 14;

QY 14 IPTVVGIFSAFGLVFTVSLFAWICQ-----RKSSKSNKTPPKYKVF----- 54
DB 16 VPAILGLTAA-----AVLSVACICARQWRLNKKQSDHSAFPQTPRPTAVRSPSQGP 71
QY 55 -HVLKGVDIYPENLNKSKKFGAADDKNVKNKPAVFN-----SLHLDLKRDNLNG 103
DB 72 PHYLK-----SPSPGTGKQMGLLSPMQDQSTSPIAQPNVKYSEEGDPAQHAEEQ-----NG 124
QY 104 N-----FKTNILKPGSPSDLENATPKLFLEGEKE-SVSPESLKSTSLTSEBQKQKGLTFL 158
DB 125 NQLTVVDGNGLKHSLNLSHSPVETIANGSVTTTLDHSLTNGKLTVTVDYQYKGLTIY 184
QY 159 FSLEYNEFERKAFVNVNIKEARGLPAWDRSQMT-----SDPIKMTILPEKKH 204
DB 185 FKRYLAERNALMVSITRCRLGPKCGSSGTGDIPTGMNGRTQATDPYVKQLLPDKQH 244
QY 205 KVTRVLRKTLDPAFDETFYGIPTQIQELALHFTILSDFRSRDDIICEVILPLSGI 264
DB 245 KVTRVVRNTPVYDDETFYGLNMNDLQNMSLHFVILSDFRSRDDIIGEVVCPHFSI 304
QY 265 E---LSEGRKMLMNRRIIKRNV-KSSGRGELLISLCYQSTTNLTVVVLKARHLPKSDVS 320
DB 305 EIGDISKEALSIKEIQPRSLKIRAQGRGELLISLCWQPAAGRLTVLLKARNLPRMVD 364
QY 321 GLSDPYVKNVLYHAKRKISKKTHVKKCTPNAFVNFVFDIP-CEG-----LEDISVEFL 375
DB 365 GLADPYVKIYLLNGORIAKKTHTVKTLSPVFNESFAFDIPAAEGAGASLEGVSL 424
QY 376 VLDSERGSNEVIGQLVGLAA-AEGTGEHWEKICDYPRIAKWHVL 422
DB 425 LLDWDRVTKNEVIGRLGELGPNSSSTALNHNWVNCSPRQIAEWHKL 472

RESULT 8
Q9U6P7 PRELIMINARY; PRT; 474 AA.
ID Q9U6P7; Q9V188;
AC Q9U6P7; Q9V188;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Synaptotagmin IV (SYTIV protein).
GN SYTIV OR CG10047.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99394599; PubMed=10466723;
RA Littleton J.T., Sereno T.L., Rubin G.M., Chapman E.R., Ganetzky B.;
RT "Synaptic function modulated by changes in the ratio of synaptotagmin I and IV";
RL Nature 400:757-760 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek J.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,


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Db 303 TVLDYRMGNKNDVIGRLILG--CNGTGAEHLHSDMLSPRRPFIQAQWHTL 350
RESULT 10
Q62747
ID Q62747 PRELIMINARY; PRT; 403 AA.
AC Q62747;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Synaptotagmin VII (Synaptotagmin VIIIS).
GN SYTVII.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=95312080; PubMed=7791877;
RA Li C., Ullrich B., Zhang J.Z., Anderson R.G., Brose N., Sudhof T.C.;
RA "Ca(2+)-dependent and -independent activities of neural and non-neural
RT synaptotagmins.";
RL Nature 375:594-599 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Sugita S., Han W., Butz S., Fernandez-Chacon R., Lao Y., Sudhof T.C.;
RT "Synaptotagmin VII as a plasma membrane Ca2+ sensor in exocytosis.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL; U20106; AAA8725.1; -.
DR EMBL; AF336854; AK01449.1; -.
DR HSSP; P21707; IRSY.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR InterPro; IPR001565; Synaptotagmin.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00399; SYNAPTOTAGMN.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS00499; C2_DOMAIN_1; 2.
DR PROSITE; PS50004; C2_DOMAIN_2; 2.
DR PROSITE; PS50004; C2_DOMAIN_2; 2.
SQ SEQUENCE 403 AA; 45482 MW; 3153FD7FC1DBEEFB CRC64;

Query Match 28.5%; Score 627.5; DB 11; Length 403;
Best Local Similarity 36.2%; Pred. No. 4, 7e-38;
Matches 153; Conservative 72; Mismatches 127; Indels 71; Gaps 11;

QY 27 VFTVSI-----FAMIC--CORKSSKNKTPPYKVFHVLKGVDIYPENLNKKKFGADD-- 77
Db 23 IITVSLVTVILCGLCHWCQKLGKRYK-----NSLETVTGTPDSG 62
QY 78 -----KNEVK-----NKPVPKNSLHLDLSEKRLDNGNPPKTNLKPSPDLENATPKLF 124
Db 63 RGRGKKAIKLPAGKAVNATPVPGQTPHDESRR-----TEPRS-----SVSDLVN--- 109
QY 125 LFLEGEKSVSPESLKSSTSLTSEE-----KQKLGTLFLESLEVNPERKAFVNIKARG 179
Db 110 -----SLTSEMMLSPGSEDEAHEGSRNLRGIRQFSVGNFOESTLTVKVMKAQE 161
QY 180 LPAMDEQSMSTDPYIKMTLPKKHKVTRVLRKTLDPADFETFTFYGIPYTOQLALHFTLSFDRFS 239
Db 162 LPKAD-FSGTSPDFVKIYLLPKKKHLETKYKKNLNPWNHETLFLFGFFYKVVQIRLY 220
QY 240 FTILSFDRPSDDITGEVLIPISGIELSEKGMMLNREIIRNVRKSSGRGELLISLCYQS 299
Db 221 LQVLVDYRFRNDPIGEVSIPLNKVLTQ--MPTFKDLKPCSDSGSGSRGELLISLCYNP 278
QY 300 TTNTLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKRKISKKTHVKCTPNVFNELFV 359
Db 279 SANSIIVNIIKARNLKAMDIGTSDPYKVMWMDKRVKKEKKTIVTKRNINLPIENESFA 338
QY 360 FDIPEGLEDISVEFLVLDSEGRSNEVIGQLVLGAAAGTGGHWNKEICDYPFRQIAKW 419
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Db 339 FDIPEKLRRTIITIVMDKOKLSRNDVIGKIYLSWKSQGEVKHWDMLTARPPQVAQW 398
QY 420 HVL 422
Db 399 HQL 401

RESULT 11
Q25393
ID Q25393 PRELIMINARY; PRT; 424 AA.
AC Q25393;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Synaptotagmin.
OS Loligo pealeii (Longfin squid).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Loliginidae; Loligo.
OX NCBI_TaxID=6621;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Optic lobe;
RX MEDLINE=9606684; PubMed=7479868;
RA Mikoshiba K., Fukuda M., Moreira J.E., Lewis F.M.T., Sugimori M.,
RA Niinobe M., Ilinas R.;
RT "Role of the C2A domain of synaptotagmin in transmitter release as
RT determined by specific antibody injection into the squid giant synapse
RT preterminal.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10703-10707 (1995).
CC -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL; D63797; BAA09866.1; -.
DR HSSP; P21707; IRSY.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR InterPro; IPR001565; Synaptotagmin.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00399; SYNAPTOTAGMN.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS00499; C2_DOMAIN_1; 2.
DR PROSITE; PS50004; C2_DOMAIN_2; 2.
DR PROSITE; PS50004; C2_DOMAIN_2; 2.
SQ SEQUENCE 424 AA; 47656 MW; F9733D3B10CFF3C0 CRC64;

Query Match 28.5%; Score 627; DB 5; Length 424;
Best Local Similarity 34.6%; Pred. No. 5, 5e-38;
Matches 144; Conservative 75; Mismatches 137; Indels 60; Gaps 8;

QY 10 EFDEIPTVVGIFSAFGLVFTVSLFAMTCCORKSSKNKTPPYKVFHVLKGVDIYPENLNS 69
Db 59 ELEKLPIMAILITCAGVLLFLVCGTYCCCKRRCRRGK----- 96
QY 70 KKKFGADDADNEKVNKPAVPKNSLHLDLSEKRLDNGNPPKTNLKPSPDLENATPKLF 129
Db 97 -----KDGKKGLKGA-----VDLKGVLGNSIKKQVP-----DLEEL----- 130
QY 130 EKESVSPESLKSSTSLTSEEKQKLGTLFLESLEVNPERKAFVNIKARGLPAMDEQSM 189
Db 131 -----PMWNEDEDAESTKSEVKLGKLYSMDYDFQKGLTVNVIQAADLPQMD-MSGT 183
QY 190 SDPYIKMTLPKKHKVTRVLRKTLDPADFETFTFYGIPYTOQLALHFTLSFDRFS 249
Db 184 SDPYKVKVLMPPDKKKFETKVRKTLNPNVNESFTFNKNFYADITGKTLFAIYDFDRFS 243
QY 250 RDDITGEVLIPUSGIELSEKGMMLN-REIK--RNVRKSSGRGELLISLCYSTNTILTY 306
Db 244 KHDQIGQVQVAMNSIDL--GSVMEERDLTSPNDAEKENKLGDI CFSRLYVPTAGKITV 301
QY 307 VVLKARHLPKSDVSGLSDPYKVNLYHAKRKISKKTHVKCTPNVFNELFV 366
Db 302 VILEAKNLKMDVGLSDPYKVISLMLNGKRIKKKTKTKKCTLNPNYINESFAFEVPEFQ 361
QY 367 LEDISVEFLVLDSEGRSNEVIGQLVLGAAAGTGGHWNKEICDYPFRQIAKWHL 422
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Db 362 IQKVSIVTVVDYDRJGTSEPTGRTFLGCSNVTGTLRHWSMDMLANPRPFAQWHTL 417
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 Q9VQG7 PRELIMINARY; PRT; 474 AA.
 ID Q9VQG7
 AC Q9VQG7
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE SVT protein.
 GN SVT OR CG3139.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
 RA Durbin K.J., Evangelisti C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spiers E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svendsen R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 CC -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
 DR EMBL; AF003582; AAF51205.1; -.
 DR HSSP; P21707; 1BYN.
 DR FlyBase; FBgn004242; svt.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002149; IRLI.
 DR InterPro; IPR001565; Synaptotagmin.
 DR Pfam; PF00168; C2; 2.
 DR PRINTS; PR00360; C2DOMAIN
 DR PRINTS; PR00339; SYNAPTOTAGMN.
 DR SMART; SM00239; C2; 2.
 DR PROSITE; PS00499; C2 DOMAIN 1; 2.
 DR PROSITE; PS00004; C2 DOMAIN 2; 2.

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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:11:10 / Search time 20 Seconds
(without alignments)
2043.584 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREDFEIPVVG.....KEICDVRQIAKHWVLCOG 425

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2006	91.1	425	2	159355
2	627.5	28.5	403	2	S58400
3	623.5	28.3	474	1	BMFR5Y
4	621	28.2	403	2	S33318
5	603.5	27.4	422	1	BMK72Y
6	603.5	27.4	422	2	A55417
7	603	27.4	511	2	S58399
8	594.5	27.0	537	2	JH0415
9	594	27.0	441	2	A40707
10	592	26.9	498	2	PC6300
11	581	26.4	422	1	BMH01Y
12	581	26.4	422	2	A45486
13	579.5	26.3	427	2	JH0413
14	577	26.2	421	2	S09595
15	575	26.1	424	2	I51210
16	574.5	26.1	439	2	JH0414
17	573.5	26.1	386	2	I59387
18	544.5	24.9	279	2	S58402
19	544.5	24.7	390	2	T28967
20	520	23.6	588	2	A53563
21	474	21.5	474	2	S68695
22	430.5	19.6	412	2	JC4921
23	415	18.9	257	2	T16355
24	408	18.5	704	2	A48097
25	394.5	17.9	681	2	JX0338
26	393.5	17.9	684	2	I58166
27	390.5	17.7	315	2	T32059
28	384.5	17.5	400	2	JC2473
29	377.5	17.2	504	2	T33485

ALIGNMENTS

RESULT 1

159355

synaptotagmin IV - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C/Accession: I59355; I58163

R/Vician, L.; Lim, I.K.; Ferguson, G.; Tocco, G.; Baudry, M.; Herschman, H.R.

Proc. Natl. Acad. Sci. U.S.A. 92, 2164-2168, 1995

A/Title: Synaptotagmin IV is an immediate early gene induced by depolarization in PC12

A/Reference number: I59355; MUID:95199312; PMID:7892240

A/Accession: I59355

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-425 <RES>

A/Cross-references: GB:I38247; NID:9598376; PIDN:AAA67327.1; PID:9598377

R/Ullrich, B.; Li, C.; Zhang, J.Z.; McMahon, H.; Anderson, R.G.; Geppert, M.; Sudhof, T

Neuron 13, 1281-1291, 1994

A/Title: Functional properties of multiple synaptotagmins in brain.

A/Reference number: I58163; MUID:95085772; PMID:7993622

A/Accession: I58163

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-425 <RES>

A/Cross-references: EMBL:U14398; NID:9550453; PIDN:AAA68519.1; PID:9550454

C/Superfamily: synaptotagmin; protein kinase C C2 region homology

F;147-262/Domain: protein kinase C C2 region homology <KC2A>

F;281-396/Domain: protein kinase C C2 region homology <KC2B>

Query Match

Best Local Similarity 91.1%; Score 2006; DB 2; Length 425;

Matches 382; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

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Db 1 MAPITTSREDFEIPVVGIFSAFGLVFTVSLFAMICQQRKSSKNKTPPYKPVHVLKGV 60

QY 61 DIYPENLNSKKKGADKNVKNKPAVKNLSHLHLDLEKRDNGNPPKTNLKPSPSDLEN 120

Db 61 DIYPENLNSKKKGADKNVKNKPAVKNLSHLHLDLEKRDNGNPPKTNLKPSPSDLEN 120

QY 121 ATPKFLFLEGEKESVSPESLKSSTLSEKQKLGTLFFSLEYNPERKAFVNNIKEARGL 180

Db 121 ATPKFLFLEGEKESVSPESLKSSTLSEKQKLGTLFFSLEYNPERKAFVNNIKEARGL 180

QY 181 PAMDEQSMTSDPIYKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGTPTQIQELALHF 240

Db 181 PAMDEQSMTSDPIYKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGTPTQIQELALHF 240

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Db 241 TVLSDFRFRDDVIGEVLPVLSGIELSDGKWLMTREIIKNAKSSGRGELLVSLCYOST 300

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:11:10 / Search time 20 Seconds
(without alignments)
2043.584 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREDFEIPVVG.....KEICDVRQIAKHWVLCOG 425

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2006	91.1	425	2	159355
2	627.5	28.5	403	2	S58400
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4	621	28.2	403	2	S33318
5	603.5	27.4	422	1	BMK72Y
6	603.5	27.4	422	2	A55417
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9	594	27.0	441	2	A40707
10	592	26.9	498	2	PC6300
11	581	26.4	422	1	BMH01Y
12	581	26.4	422	2	A45486
13	579.5	26.3	427	2	JH0413
14	577	26.2	421	2	S09595
15	575	26.1	424	2	I51210
16	574.5	26.1	439	2	JH0414
17	573.5	26.1	386	2	I59387
18	544.5	24.9	279	2	S58402
19	544.5	24.7	390	2	T28967
20	520	23.6	588	2	A53563
21	474	21.5	474	2	S68695
22	430.5	19.6	412	2	JC4921
23	415	18.9	257	2	T16355
24	408	18.5	704	2	A48097
25	394.5	17.9	681	2	JX0338
26	393.5	17.9	684	2	I58166
27	390.5	17.7	315	2	T32059
28	384.5	17.5	400	2	JC2473
29	377.5	17.2	504	2	T33485


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QY 301 TMTLVVVLKARHLPKSDVSGLSDPYKVNLYHAKRIISKKTHVKKCTPNVAFNELVVF 360
DB 301 TMTLVVVLKARHLPKSDVSGLSDPYKVNLYHAKRIISKKTHVKKCTPNVAFNELVVF 360
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QY 421 VLCDG 425
DB 421 MLCDG 425

RESULT 2
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cellotagmin II sytVII - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 13-Aug-1999
C:Accession: S58400
R;Li, C.; Ullrich, B.; Zhang, J.Z.; Anderson, R.G.W.; Brose, N.; Suedhof, T.C.
Nature 375, 594-599, 1995
A:Title: Ca(2+)-dependent and -independent activities of neural and non-neural synaptotagmin
A:Reference number: S58399; MUID:95312080; PMID:7791877
A:Accession: S58400
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <LIC>
A:CROSS-references: EMBL:U20106; NID:G643655; PIDN:AAA87725.1; PID:G643656
C:Superfamily: synaptotagmin; protein kinase C C2 region homology
F;129-243/Domain: protein kinase C C2 region homology <KC2A>
F;260-375/Domain: protein kinase C C2 region homology <KC2>

Query Match 28.5%; Score 627.5; DB 2; Length 403;
Best Local Similarity 36.2%; Pred. No. 3.8e-36;
Matches 153; Conservative 72; Mismatches 127; Indels 71; Gaps 11;

QY 27 VFTVSL-----FAWIC--CORKSSKNTPPYKFVHLKGVLDIYPENLNSKKKFGADD-- 77
DB 23 IITVSLVTIVLCGLCHWCQKRLGRYK-----NSLETGVTGPDG 62
QY 78 -----KNEVK-----NKPAVPKNSLSHLDEKRLDNGNFKTNLKPSPSLENATPK 124
DB 63 RGRGEKKAIKLPAGGKAVNTAPVPGTQPHDESDRR-----TEPRS-----SVSDLVN-- 109
QY 125 LFLGEXESVSPESIKSSTLSLSE-----KQKGLTLFSLFYNEPFAFVNIKEARG 179
DB 110 -----SLTSEMMLSPGSEDEAHEGCSRENIGRIQFSVGNFQESTLTIVKVMKAQE 161
QY 180 LPAMDEQMSSTDPIKMTILPEKKHKVTRVLRKTLDPAPDETFTFYGIPYTOIELALH 239
DB 162 LPAKD--FSGTSDPFVKIYLLPDKKHLETQVKRKNLNPWNTEFLFEGFPYKVVQRILY 220
QY 240 FTILSPFRSDDDIIGEVLPLSGTELSEGMMLMREIIRKRVNKSRSRGELLISLCYQS 299
DB 221 LQVLDDYRFRSNDPIGEVSIPLNKVDLTQ--MOTFWKDLKPCSDGSGRSELLSLCYNP 278
QY 300 TMTLVVVLKARHLPKSDVSGLSDPYKVNLYHAKRIISKKTHVKKCTPNVAFNELFV 359
DB 279 SANSIIVNIIKARNLKAMDIGTSDPYKVMWLMYKDKRVEKKTKVTKRNLNIPFNESFA 338
QY 360 FDPICEGLIEDISVEFLVLDSEGRNEVIGQLVLGAAAGTGGHWEKEICDYPFRQIAKWH 419
DB 339 FDIPEKURETIIITVMDKDLNSRDVIGKLYLSWKSGPGEVGHKWDMIARPRQPAQW 398
QY 420 HVL 422
DB 399 HQL 401

RESULT 3
BMFFSY
synaptotagmin - fruit fly (Drosophila melanogaster)
N;Alternate names: p65
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C:Species: Drosophila melanogaster
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C:Accession: B39052
R;Perin, M.S.; Johnston, P.A.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 266, 615-622, 1991
A:Title: Structural and functional conservation of synaptotagmin (p65) in Drosophila ar
A:Reference number: A39052; MUID:91093190; PMID:1840599
A:Accession: B39052
A:Molecule type: mRNA
A:Residues: 1-474 <PER>
A:CROSS-references: GB:M55048; GB:J05711; NID:G158526; PIDN:AAA28925.1; PID:G158527
C:Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are t
C:Genetics:
A:Gene: FlyBase:syt
A:CROSS-references: FlyBase:FBgn0004242
A:Map position: 23B
C:Superfamily: synaptotagmin; protein kinase C C2 region homology
C:Keywords: duplication; membrane trafficking; phospholipid binding; synaptic vesicle;
F;1-107/Domain: intravesicular #status predicted <INT>
F;108-134/Domain: transmembrane #status predicted <TM>
F;135-474/Domain: extravesicular #status predicted <EXT>
F;186-434/Region: phospholipid binding #status experimental
F;186-300/Domain: protein kinase C C2 region homology <KC2A>
F;319-434/Domain: protein kinase C C2 region homology <KC2B>

Query Match 28.3%; Score 623.5; DB 1; Length 474;
Best Local Similarity 34.9%; Pred. No. 9.2e-36;
Matches 152; Conservative 66; Mismatches 144; Indels 73; Gaps 9;

QY 3 PITTSREDFRIPVTV-----GIFSAGLVFTVSLFAWICQKSKSNKNTPPYK 52
DB 88 FVIKKIHVGEVTVTEVIAERTGLPTWGVVAIIILVFLVFGIIFFCVRRFLKKRTK-- 144
QY 53 FVHLKGVLDIYPENLNSKKKGADDKNEVKNKPAVPKNSLSHLDEKRLDNGNFKTNLKP 112
DB 145 -----DGRGKKG-----VDMKSVQLLGSAKKEVQVP 170
QY 113 GSPSDLENATPKLLEGEKESVSPESIKSSTLSITSEKQKGLTLFSLFYNEPFAFV 172
DB 171 DMEELTENAE-----EGDEE-----DKSQKQLRLNPKLEYDFNNSLAV 211
QY 173 NIKEARGLPAMDQMSSTDPIKMTILPEKKHKVTRVLRKTLDPAPDETFTFYGIPY 232
DB 212 TVIQAELPALD--MGTSDDPYKVVLLPDKKKFKETKVRKLTSPVFNETFTPKSLPYAD 270
QY 233 IQELALHTIILSPFRSDDDIIGEVLPLSGTELSEGMMLMREIIRKRVNKSRSR--G 289
DB 271 AMNKTLPFAIFDFRFSKHDQIGEVKVPCLCTIDLAQ--TIEWRDLV--SYEGEGGQKLG 327
QY 290 ELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKRIISKKTHVKKCT 349
DB 328 DICFSLRVPTAGKUTVVVILEAKNKKMDVGLSDPYVKIATMONGKRLKKKTSVKCT 387
QY 350 PNAVNELFVDIPCEGLIEDISVEFLVLDSEGRNEVIGQLVLGAAAGTGGHWEKEIC 409
DB 388 LNPYNESFSEVPPEQMKICLVTVVDYDRLGITSEPIGRCILGCMGTGTELHWSMDL 447
QY 410 DYPRRQIAKWHVLC 424
DB 448 ASRRPIAQWHTLKD 462

RESULT 4
S33318
synaptotagmin - longfin squid
C:Species: Loligo pealeii (longfin squid)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
C:Accession: S33318
R;Bommert, K.; Charlton, M.P.; DeBello, W.M.; Chin, G.J.; Betz, H.; Augustine, G.J.
Nature 363, 163-165, 1993
A:Title: Inhibition of neurotransmitter release by C2-domain peptides implicates synapt
A:Reference number: S33318; MUID:93247639; PMID:8097867
A:Accession: S33318
```

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-403 <BM>
C;Cross-references: EMBL:X72386; NID:g311734; PIDN:CAA51079.1; PID:g311735
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
F;121-235/Domain: protein kinase C C2 region homology <KC2A>
F;255-370/Domain: protein kinase C C2 region homology <KC2B>

Query Match 28.2%; Score 621; DB 2; Length 403;
Best Local Similarity 35.6%; Pred. No. 1.1e-35;
Matches 149; Conservative 71; Mismatches 131; Indels 68; Gaps 10;

QY 10 EFDEIPITVVGIFSAFGLVFTVSLFAWICQ---RKSSKSNKTPPYKFVHVHLKGVDPEN 66
DB 40 ELEKLPITWAILICAGVLLFVCGTYCCCKRICRRGKXKDGKGLGAGVLDLGVQLL--- 96
QY 67 LNSKKKFGADDKNEVKNKPAVFNKSLHLDLKRDNLNGNPKTNLKPSPDLENATPKLF 126
DB 97 -----GNSIKEXP-----DLEELPMN-----MEDNEDA----- 119
QY 127 LEGKESVSPSLKSSSTSLTSEKQKGLTLPFSLFYNFERKAFVNVNIKEARGLPAMDEQ 186
DB 120 -----ESTKS-----EVKLGKIQVMDYDFQKGLTNNVLIQAADLPQMD-M 159
QY 187 SMTSDPYIKMTILPEKKHKVTRVRLKTLDPADFTFTFYGIPYTOIQELALHFTILSPD 246
DB 160 SGTSDPYVKKVYVLPDQKKKFKETKVRKTLNPNVFNESFTFNVPYADITGKTLVFAIYDFD 219
QY 247 RFSRDDIIGEVLIPLSGIELSGLKLMN-RELIK--RNVKSSGRGELLISLCYQSTTNT 303
DB 220 RFSKHDQIGQVQVAVNSIDL--GSVWEERDITSPDDAEKENKLGIDICFSLYRVPAGK 277
QY 304 LTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTPNVAFNELFVFDIP 363
DB 278 LTVVILEAKNLLKMDVGLSDPYKVISLMLNGRIKKKTKTKTLNPNYNSFAFEVP 337
QY 364 CEGLEDISVEFLVLDSEGRSNEVIGQLVGLAAAGTGGEHKEICDYPRRQIAKHVHL 422
DB 338 FEQIQKSLYTVVVDYDRHTWTEPIGRTELGCSNLTGTLRHNSDMLANPRPIAQHWTL 396

RESULT 5
BMRT2Y
synaptotagmin II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A39454
R;Geppert, M.; Archer III, B.T.; Suedhof, T.C.
J. Biol. Chem. 266, 13548-13552, 1991
A;Title: Synaptotagmin II. A novel differentially distributed form of synaptotagmin.
A;Reference number: A39454; MUID:91310620; PMID:1856191
A;Accession: A39454
A;Molecule type: mRNA
A;Residues: 1-422 <GEP>
C;Cross-references: GB:M64488; NID:g207144; PIDN:AAA63502.1; PID:g207145
C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are the C;Superfamily: synaptotagmin; protein kinase C C2 region homology
F;1-60/Domain: duplication; glycoprotein; membrane trafficking; phospholipid binding; synap F;61-87/Domain: intravesicular #status predicted <INT>
F;88-422/Domain: transmembrane #status predicted <TM>
F;136-382/Region: phospholipid binding #status predicted
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2B>
F;32/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.4%; Score 603.5; DB 1; Length 422;
Best Local Similarity 35.6%; Pred. No. 1.9e-34;
Matches 151; Conservative 63; Mismatches 127; Indels 83; Gaps 12;

QY 10 EFDEIPITVVGIFSAFGLVFTVSLFA---WICQKSSKSNKTPPYKFVHVHLKGVDI 62
DB 57 EINKIPLPPWALIAMAVVAGLLLTCCFCICCKCKCKKKNKKEKG-----KGM-- 105

QY 63 YPENLNSKKKFGADDKNEVKNKPAVFNKSLHLDLKRDNLNGNPKTNLKPSPDLENAT 122
DB 106 -KNAMNMKMDKGGQDDDDA-----ETGLTEG----- 130
QY 123 PKLFLLEGKESVSPSLKSSSTSLTSEKQKGLTLPFSLFYNFERKAFVNVNIKEARGLP 182
DB 131 -----EGEGE-----EKEPENLGKIQFSLDYDFQANQLTVGVLOAAELPA 171
QY 183 MDEQSMSTDPYIKMTILPEKKHKVTRVRLKTLDPADFTFTFYGIPYTOIQELALHFTI 242
DB 172 LD-MGTSDDPYVKKVLPDQKKKFKETKVRKTLNPNVFNESFTFNVPYADITGKTLVMAI 229
QY 243 LSFDRSDDIIGEVLIPLSGIEL-----SEKMLMNRRIIKRNVKSSGRGELLISLCYQ 298
DB 230 YDFDRFSKHDITIGEVKVPMTVLDGQPIEWRDLQGE--KEEPEK--LGDICTSLRYV 284
QY 299 STTNLTITVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTPNVAFNELF 358
DB 285 PTAGKLTVCILEAKNLLKMDVGLSDPYKVIHLQMONGKRLKKKTKTKTKTLNPNYNSF 344
QY 359 VFDIPCEGLEDISVEFLVLDSEGRSNEVIGQLVGLAAAGTGGEHKEICDYPRRQIAK 418
DB 345 SFEIPFEQIQKVVVVTVLDYDKLGKNEALGKIFVGSNAIGTELHRHNSDMLANPRPIAQ 404
QY 419 WHVL 422
DB 405 WHSL 408

RESULT 6
A55417
synaptotagmin II - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 07-Jun-1996
C;Accession: A55417; B39454
R;Fukuda, M.; Aruga, M.; Nimobe, M.; Aimoto, S.; Mikoshiba, K.
J. Biol. Chem. 269, 29206-29211, 1994
A;Title: Inositol-1,3,4,5-tetrakisphosphate binding to C2B domain of IP4BP/synaptotagmin.
A;Reference number: A55417; MUID:95050743; PMID:7961887
A;Accession: A55417
A;Molecule type: mRNA
A;Residues: 1-422 <FUK>
C;Cross-references: GB:D37792; GB:D37793
R;Geppert, M.; Archer III, B.T.; Suedhof, T.C.
J. Biol. Chem. 266, 13548-13552, 1991
A;Title: Synaptotagmin II. A novel differentially distributed form of synaptotagmin.
A;Reference number: A39454; MUID:91310620; PMID:1856191
A;Accession: B39454
A;Molecule type: DNA
A;Residues: 377-422 <GEP>
C;Cross-references: GB:M64488
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: membrane trafficking
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2B>

Query Match 27.4%; Score 603.5; DB 2; Length 422;
Best Local Similarity 35.6%; Pred. No. 1.9e-34;
Matches 151; Conservative 63; Mismatches 127; Indels 83; Gaps 12;

QY 10 EFDEIPITVVGIFSAFGLVFTVSLFA---WICQKSSKSNKTPPYKFVHVHLKGVDI 62
DB 57 EINKIPLPPWALIAMAVVAGLLLTCCFCICCKCKCKKKNKKEKG-----KGM-- 105
QY 63 YPENLNSKKKFGADDKNEVKNKPAVFNKSLHLDLKRDNLNGNPKTNLKPSPDLENAT 122
DB 106 -KNAMNMKMDKGGQDDDDA-----ETGLTEG----- 130
QY 123 PKLFLLEGKESVSPSLKSSSTSLTSEKQKGLTLPFSLFYNFERKAFVNVNIKEARGLP 182
DB 131 -----EGEGE-----EKEPENLGKIQFSLDYDFQANQLTVGVLOAAELPA 171

A;Residues: 1-441 <NON>
A;Cross-references: GB:L15302; NID:g289717; PIDN:AAA28145.1; PID:g289718
R;Dt, Z.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F31E8.
A;Reference number: Z18481
A;Accession: T16226
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-441 <DUZ>
A;Cross-references: EMBL:U55856; NID:g1280154; PID:g1280158; PIDN:AAA98023.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone F31E8
C;Genetics:
A;Gene: snt-1
A;Map position: 2
A;Intons: 39/2; 72/1; 132/3; 289/3; 329/1; 373/3; 408/2
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: membrane trafficking; transmembrane protein
F;153-266/Domain: protein kinase C C2 region homology <KC2A>
F;286-401/Domain: protein kinase C C2 region homology <KC2B>
Query Match 27.0%; Score 594; DB 2; Length 441;
Best Local Similarity 40.2%; Pred. No. 9.3e-34;
Matches 148; Conservative 57; Mismatches 111; Indels 52; Gaps 14;
QY 70 KKFGGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPK-----TNLKPGSPSDLENAT 122
DB 97 RKLFGKKHGE-KNK-----KGGKGGFGKGQDVVDGKNIQ-GMAQDLIELG 141
QY 123 PKLFLGEGESVSPESLSKSTSLTSEKQE-KLGLTFLFSLEYNFPERKAFVNIKEARGLP 181
DB 142 DAM-EQNEKEQ-----AEEKEVKGRIQYKLDYDFOGQQLTVTVIQAEDLP 187
QY 182 AMDEQSMTPSYIKMTILPEKKHKVKTSLVRLTDPAPDETETFFGIPYQIQELAHHT 241
DB 188 GMD-MGSTDPYVKLYLLPEKKKVKVETVHRKTLNPNVFNETPIF-KVAFNEITAKTLVPA 245
QY 242 ILSDFRSDRDIIIGEVLPILSGIELSEKMLMNRIL-----KRVNRKSSGGELLISLC 296
DB 246 IYDFRFSKHDQIQVILPGLKIDL--GAVIEWKDIAPPPDDKEAKS--LGDICFSLR 301
QY 297 YQSTNTTLTVVILKARHLPSKSDVSGLSDPYVKNLYHAKRISKKKTHVKKCTPNVAFNE 356
DB 302 YVPTAGKLTVILEAKNLKMDVGLSDPYVKIVLMQGGKRLKKKTSIKKTLNPNYNE 361
QY 357 LFVFDIPCEGLEDSVLELVLDSEGRSNEVIGQLVGAABEGTGE--HWKEICDYPRR 414
DB 362 SFSFEVPFEQIQVSLMITVMDYDKLSNDAIGRCLLG--CNGTGAEILRHWMMLASPRR 419
QY 415 QIAKWHVL 422
DB 420 PIAQWHTL 427
RESULT 10
PC6300
synaptotagmin X - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C;Accession: PC6300
R;Babity, J.M.; Armstrong, J.N.; Plumier, J.C.L.; Currie, R.W.; Robertson, H.A.
Proc. Natl. Acad. Sci. U.S.A. 94, 2638-2641, 1997
A;Title: A novel seizure-induced synaptotagmin gene identified by differential display.
A;Reference number: PC6300; MUID:97226006; PMID:9122248
A;Accession: PC6300
A;Molecule type: mRNA
A;Residues: 1-498 <SAB>
A;Cross-references: GB:U85513; NID:g1932800; PIDN:AA851686.1; PID:g1932801
C;Comment: This protein responses to seizure activity.
C;Genetics:
A;Gene: svt X
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: transmembrane protein

F;56-77/Domain: transmembrane #status predicted <TMM>
F;74-224/Domain: cytoplasmic #status predicted <CRY>
F;224-338/Domain: protein kinase C C2 region homology <KC2>
F;357-472/Domain: protein kinase C C2 region homology <KC2B>
Query Match 26.9%; Score 592; DB 2; Length 498;
Best Local Similarity 34.6%; Pred. No. 1.5e-33;
Matches 158; Conservative 72; Mismatches 156; Indels 70; Gaps 16;
QY 20 IFSAFGL-VFTVSLFA-WTCQCKSSKSNKTPPYKPVHLKGVVDIYENLNS--KKKFGA 75
DB 60 VVSCGLALLVSLVFWKLC-----WPCWKSILVAPNVSTLPQSISAPTEVFT 110
QY 76 DDKNEV-KNKPAVPKNSLHLDLEKRDINGNFP-----KTNLK-----PGSPS 116
DB 111 EEKKEVENKPAK-ALEPAIKISHTSPDIAEVQTALKEHLKHARVORQTTDPTSSS 169
QY 117 -----DLENATPKLFLGEEKS-----VSPESLSKSTSLTSE-----EK 150
DB 170 RHNSFRRLPQMNVSVDVFSMGTPVLQGRTRTSIGRIKPELYKQK-SVDSEGNKDD 228
QY 151 QEKLGTLFFSLEYNFERKAFVNIKEARGLPAMDEQSMTPSYIKMTILPEKKHKVKTIV 210
DB 229 VKTCGLNFALQYDENELVVVKIIKALDLPKADSTG-TSDPYVKIYLLPDRKKKQFQTV 287
QY 211 LRKTLDPADFDTFTFYGIPYQIQELAHHTILSDFRSDDIIIGEVILPLSGIELSEK 270
DB 288 HRKTLNPLDFELQF-PVYDQLSNRKLHFSIYDFDRSRHDMIGEVL-----NLFVS 342
QY 271 MLNREIIRKVR-----KSSGRGELLISLCYSTNTTLTVVILKARHLPSKSDVSGLSDPY 326
DB 343 DLSREATWKDIHCATTESMDLGEIMFSLCYLPTAGRMILTIVIKCNLKMADITGSSDPY 402
QY 327 VKNLYHAKRISKKKTHVKKCTPNVAFNELVFDIPCEGLEDSVLEFVLDSERGRNE 386
DB 403 VKVSLMCEGRLLKRRKKTTKNTLNPVYNEAIFDIPPENVDQVSLCIAVMDYDRVGHNE 462
QY 387 VIGQLVGAABEGTGEHWKELCIDYPRQIAKWHVL 422
DB 463 VIGVCRGTGLDAEGLGRDHWNEMLAYHRKEITHWHEL 498
RESULT 11
BMHUY
synaptotagmin I - human
N;Alternate names: p65
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A39052
R;Perin, M.S.; Johnston, P.A.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 266, 615-622, 1991
A;Title: Structural and functional conservation of synaptotagmin (p65) in Drosophila and
A;Reference number: A39052; MUID:91093190; PMID:1840599
A;Accession: A39052
A;Molecule type: mRNA
A;Residues: 1-422 <PER>
A;Cross-references: GB:M55047; GB:J05710; NID:g338657; PIDN:AAA60609.1; PID:g338658
C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are th
C;Genetics:
A;Gene: GDB:SYT1; SYT
A;Cross-references: GDB:125296; OMIM:185605
A;Map position: 12cen-12q21
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: dimer; duplication; glycoprotein; membrane trafficking; phospholipid binding
F;1-53/Domain: intravesicular #status predicted <INT>
F;51-80/Domain: transmembrane #status predicted <TMM>
F;81-422/Domain: extravesicular #status predicted <EXT>
F;136-382/Region: phospholipid binding #status experimental
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2B>
F;25/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 26.4%; Score 581; DB 1; Length 422;

Best Local Similarity 39.9%; Pred. No. 7e-33;
Matches 132; Conservative 65; Mismatches 114; Indels 20; Gaps 8;
QY 105 FPKTNLPGSPDLLENATPKLFLGEGKESVPSLSK---SSTSLT-SEEK-----QKLG 155
DB 85 FKKNNKKKGGKGNAINMKDKLGKTKMDQALDQDAETGLTGDEEKEEPEEKLK 144
QY 156 TLFFSLEYNFERKAFVNNIKERAGLPAMDQSMSTDPYIKMTILPEKKHKVTRVLKRTL 215
DB 145 KLOYSLDYDFQNNQLLVGIIQAELPALD-MGGTSDPYVVKVFLPDKKKKFKTKVHRKTL 203
QY 216 DPAFDETFFYGIPTQIOELALHFTILSFDRSRDDIIGEVLIPLSGIEL-----SEGKM 271
DB 204 NPVNEQFTF-KVPYSELGGKTLVMAVYDFDRFSKHDIIIGEFKVPMTVDFGHVTEWRD 262
QY 272 LMNREIIKRNVRKSSGRGELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYVKVNL 331
DB 263 LOSAE--KEEQEK---LGDICFSLRYVPTAGKTUTVILEAKNLKMDVGGSLDPYVKIHL 317
QY 332 YHAKKRISKKTHVKCTPNVFNELFVDIPCEGLEDISVEFLVLDSEGRSNEVIGQL 391
DB 318 MONGKRLKKKTKTKNTLNPYNESFSEVPPEQIQKVQVVTVLDYDKIGNDAIGKV 377
QY 392 VLGAAGTGGGHEHKEICDYPRIQIAKHVYL 422
DB 378 FVGYNSTGAELRHWSMDLANPRPIAQWHTL 408

RESULT 12

A45486
N/A: synaptotagmin I - bovine
N/Alternate names: 39K protein; synaptic vesicle protein p65
C/Species: Bos primigenius taurus (cattle)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C/Accession: A45486; S19272
R/Davilecov, B.; Sontag, J.M.; Hata, Y.; Petrenko, A.G.; Fykse, E.M.; Jahn, R.; Sudhof, T.
J. Biol. Chem. 268, 6816-6822, 1993
A/Title: Phosphorylation of synaptotagmin I by casein kinase II.
A/Reference number: A45486; MUID:93203288; PMID:8454654
A/Accession: A45486
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-422 <DAV>
A/Cross-references: GB:L05922; NID:945210; PIDN:AAA87360.1; PID:945211
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBI:128028, NCBI:P:128029)
R/Tugal, H.B.; van Leeuwen, F.; Apps, D.K.; Haywood, J.; Phillips, J.H.
Biochem. J. 279, 699-703, 1991
A/Title: Glycosylation and transmembrane topography of bovine chromaffin granule p65.
A/Reference number: S19272; MUID:92061982; PMID:1719959
A/Accession: S19272
A/Molecule type: protein
A/Residues: 113-132 <TUG>
C/Superfamily: synaptotagmin; protein kinase C C2 region homology
F:136-249/Domain: protein kinase C C2 region homology <KC2A>
F:267-382/Domain: protein kinase C C2 region homology <KC2B>

Query Match 26.4%; Score 581; DB 2; Length 422;
Best Local Similarity 39.9%; Pred. No. 7e-33;
Matches 132; Conservative 65; Mismatches 114; Indels 20; Gaps 8;

QY 105 FPKTNLPGSPDLLENATPKLFLGEGKESVPSLSK---SSTSLT-SEEK-----QKLG 155
DB 85 FKKNNKKKGGKGNAINMKDKLGKTKMDQALDQDAETGLTGDEEKEEPEEKLK 144
QY 156 TLFFSLEYNFERKAFVNNIKERAGLPAMDQSMSTDPYIKMTILPEKKHKVTRVLKRTL 215
DB 145 KLOYSLDYDFQNNQLLVGIIQAELPALD-MGGTSDPYVVKVFLPDKKKKFKTKVHRKTL 203
QY 216 DPAFDETFFYGIPTQIOELALHFTILSFDRSRDDIIGEVLIPLSGIEL-----SEGKM 271
DB 204 NPVNEQFTF-KVPYSELGGKTLVMAVYDFDRFSKHDIIIGEFKVPMTVDFGHVTEWRD 262

QY 272 LMNREIIKRNVRKSSGRGELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYVKVNL 331
DB 263 LOSAE--KEEQEK---LGDICFSLRYVPTAGKTUTVILEAKNLKMDVGGSLDPYVKIHL 317
QY 332 YHAKKRISKKTHVKCTPNVFNELFVDIPCEGLEDISVEFLVLDSEGRSNEVIGQL 391
DB 318 MONGKRLKKKTKTKNTLNPYNESFSEVPPEQIQKVQVVTVLDYDKIGNDAIGKV 377
QY 392 VLGAAGTGGGHEHKEICDYPRIQIAKHVYL 422
DB 378 FVGYNSTGAELRHWSMDLANPRPIAQWHTL 408

RESULT 13

JH0413
N/A: synaptotagmin o-p65-A - electric ray (Discopyge ommata)
N/Alternate names: synaptic vesicle protein o-p65-A
C/Species: Discopyge ommata
C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-Aug-1999
C/Accession: JH0413
R/Wendland, B.; Miller, K.G.; Schilling, J.; Scheller, R.H.
Neuron 6, 993-1007, 1991
A/Title: Differential expression of the p65 gene family.
A/Reference number: JH0413; MUID:91273991; PMID:2054189
A/Accession: JH0413
A/Molecule type: mRNA
A/Residues: 1-427 <WEN>
A/Cross-references: GB:M64275; NID:9213108; PIDN:AAA9227.1; PID:9213109
A/Experimental source: electric organ
C/Superfamily: synaptotagmin; protein kinase C C2 region homology
C/Keywords: glycoprotein; membrane protein; membrane trafficking; synaptic vesicle
F:58-84/Domain: hydrophobic <HYD>
F:141-254/Domain: protein kinase C C2 region homology <KC2A>
F:272-387/Domain: protein kinase C C2 region homology <KC2B>
F:267/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 26.3%; Score 579.5; DB 2; Length 427;
Best Local Similarity 38.8%; Pred. No. 9.1e-33;
Matches 128; Conservative 66; Mismatches 115; Indels 21; Gaps 7;

QY 107 KTNLPGSPDLLENATPKLFLGEGKESVPSLSKSTSLTS-----EEKQEKLG 156
DB 91 KKNKKKGGKGNAINMKDKVEMGKSGEQALQALDEDAETGLTDTGKEEKEDEKLK 150
QY 157 TLFFSLEYNFERKAFVNNIKERAGLPAMDQSMSTDPYIKMTILPEKKHKVTRVLKRTL 216
DB 151 KQYSLDYDFQNNQLLVGIIQAELPALDVG--TSDPYVVKVFLPDKKKKFKTKVHRKTL 209
QY 217 DPAFDETFFYGIPTQIOELALHFTILSFDRSRDDIIGEVLIPLSGIEL-----SEGKML 272
DB 210 PVFNESFTF-KIPYSELGGKTLVMAVYDFDRFSKHDVIGAKVPMNTVDFGHVTEWRDL 268
QY 273 MNREIIKRNVRKSSGRGELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYVKVNL 332
DB 269 QGAE--KEEQEK---LGDICFSLRYVPTAGKTUTVILEAKNLKMDVGGSLDPYVKIHL 323
QY 333 HAKKRISKKTHVKCTPNVFNELFVDIPCEGLEDISVEFLVLDSEGRSNEVIGQL 392
DB 324 QNGKRLKKKTKTKNTLNPYNESFSEVPPEQIQKVQVVTVLDYDKIGNDAIGKV 383
QY 393 LGAAAGTGGGHEHKEICDYPRIQIAKHVYL 422
DB 384 VGYNSTAAELRHWSMDLANPRPIAQWHTL 413

RESULT 14

S09595
N/A: synaptotagmin P65 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Aug-1997
C/Accession: S09595; S20211
R/Perin, M.S.; Fried, V.A.; Mignery, G.A.; Jahn, R.; Sudhof, T.C.
Nature 345, 260-263, 1990

A;Title: Phospholipid binding by a synaptic vesicle protein homologous to the regulatory
A;Reference number: S09595; MUID:90238548; PMID:2333096
A;Accession: S09595
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-421 <PER1>
A;Accession: S20211
A;Molecule type: protein
A;Residues: 145-168;201-212;214-216;237-244;333-354;357-366;376-388;392-398 <PER2>
A;Note: 99-Asp, 116-Glu, 169-Arg, and 232-Glu were also found
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: calmodulin binding; glycoprotein; membrane trafficking; synaptic vesicle; tr
F;1-52/Domain: intravesicular #status predicted <INT>
F;53-79/Domain: transmembrane #status predicted <TM>
F;80-421/Domain: extravesicular #status predicted <EXT>
F;135-248/Domain: protein kinase C C2 region homology <KC2A>
F;266-381/Domain: protein kinase C C2 region homology <KC2B>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.2%; Score 577; DB 2; Length 421;
Best Local Similarity 39.9%; Pred. No. 1.3e-32;
Matches 132; Conservative 64; Mismatches 115; Indels 20; Gaps 8;

QY 105 PPKNLPKPSDLENATPKLFLEGEKESVSPESLK---SSTSILT-SEEK-----QKLG 155
DB 84 PKNKKNKKGKGGKGNAINMKDVOLGKTWKQALXDDDAETGLTDEGEKEEPKEEKLK 143

QY 156 TLFFSLEVNFERKAVVNIKEARGLPAMDQSMTPDYIKMTILPEKKHKVKTFLVLRKTL 215
DB 144 KLOYSLDYQNNQLLVGLIQAAELPALD-MOGTSDPYVVKVFLPLPKKKKFKETKVRKTL 202

QY 216 DPAFDETFYGIPTQIQLALHFTILSFRSDRIIGEVLIPLSGIEL----SEGM 271
DB 203 NPVNEQFTF-KVPSSELGGKTLVMAVYDFDRSKHDIIGEVKVPMTVDFGHVTEWRD 261

QY 272 LMNREIIKRNVRKSSGRGELLISLCYQSTNTLTIVVVLKARHLPKSDVSGLSDPYVKNV 331
DB 262 LQSAE--KEEQK---LGDICFSLRVPTAGKLTIVVLEAKNLKMDVGLSDPYVKIHL 316

QY 332 YHAKRKSKTHVKTTPNAVFNELFVFDIPCEGLEDSVEFLVLDSEGRSNEVIGQL 391
DB 317 MQNGKRLKKKTTIKKNTINPYNESFSFEVPEQIKQVQVVVTVLDYDKIGNDAIDKV 376

QY 392 VLGAAGETGGGHEHKEICDYPRIQAKHVL 422
DB 377 FVGNSTGAELRHWSMDLANPRPRPIAQWHTL 407

RESULT 15
I51210
synaptotagmin p65 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: I51210
E;Lou, X.; Bixby, J.L.
Dev. Biol. 159, 327-337, 1993
A;Title: Coordinate and noncoordinate regulation of synaptic vesicle protein genes durin
A;Reference number: I51210; MUID:93374184; PMID:8365570
A;Accession: I51210
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-424 <LOU>
A;Cross-references: GB:S64957; NID:G409527; PIDN:AAB28081.1; PID:G409528
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
F;138-251/Domain: protein kinase C C2 region homology <KC2>
F;269-384/Domain: protein kinase C C2 region homology <KC2B>

Query Match 26.1%; Score 575; DB 2; Length 424;
Best Local Similarity 37.0%; Pred. No. 1.8e-32;
Matches 141; Conservative 71; Mismatches 129; Indels 40; Gaps 11;

QY 68 NSKKKFGADDKNEVKNKPAVPPKNSLHLD-----LEKRDINGNFPKTNLKPGS 114

Db 44 NLKKKF----NMELNKIPLPPWALIAIAVAVLLILTCCFCCLKCKCL---FKKKNKKKKK 96
QY 115 PSDLENATPKLFLEGEKESVSPESLK---SSTSILT-SEEKQ-----EKGLTLPFSLEYNF 165
DB 97 EKGKGNAINMKDVOLGKTWKQALXDDDAETGLTDEGEKEEPKEVKEKLGKIQYSLDYDF 156
QY 166 ERKAFVNIKEARGLPAMDQSMTPDYIKMTILPEKKHKVKTFLVLRKTLDPADDETTF 225
DB 157 QNNQLLVGLIQAAELPALD-MOGTSDPYVVKVFLPLPKKKKYEKTKVHRKTLNPFVNEQFTF 215
QY 226 YGIPYTOIQLALHFTILSFRSDRIIGEVLIPLSGIEL----SEGM 281
DB 216 -KVPSELGGKTLVMAVYDFDRSKHDIIGEVKVPMTVDFGHVTEWRDLSAE--KEE 272
QY 282 VRKSSGRGELLISLCYQSTNTLTIVVVLKARHLPKSDVSGLSDPYVKNVLYHAKKRISK 341
DB 273 QEK---LGDICFSLRVPTAGKLTIVVLEAKNLKMDVGLSDPYVKIHLMQNGKRLKK 329
QY 342 KTHVKKCTPNVFNELFVFDIPCEGLEDSVEFLVLDSEGRSNEVIGQLVLGAAGETG 401
DB 330 KTTIKKNTINPYNESFSFEVPEQIKQVQVVVTVLDYDKIGNDAIDKGVFVGNSTGAE 389
QY 402 GEHWKEICDYPRIQAKHVL 422
DB 390 LRHWSMDLANPRPRPIAQWHTL 410

Search completed: February 20, 2004, 13:14:44
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:12:55 ; Search time 40 Seconds
(without alignments)
2224.687 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREDFEIPVTGGI.....KEICDYPRRQIAKHWLVDG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2201	100.0	425	11	US-09-954-570-2
2	1162	52.8	431	12	US-10-311-626-9
3	614	27.9	195	12	US-09-764-875-772
4	609	27.7	523	12	US-10-231-913-12
5	603	27.4	188	9	US-09-764-870-368
6	603	27.4	188	12	US-09-764-875-1072
7	603	27.4	188	15	US-10-125-540-368
8	603	27.4	461	9	US-09-764-870-365
9	603	27.4	461	15	US-10-125-540-365
10	603	27.4	511	12	US-10-231-913-82
11	598	27.2	511	12	US-10-231-913-81
12	592	26.9	498	12	US-10-231-913-80
13	590	26.8	523	12	US-10-231-913-79
14	589	26.8	523	12	US-10-231-913-78
15	581	26.4	906	12	US-10-307-389-6
					Sequence 2, Appli
					Sequence 9, Appli
					Sequence 772, App
					Sequence 12, Appl
					Sequence 368, App
					Sequence 1072, Ap
					Sequence 368, App
					Sequence 365, App
					Sequence 365, App
					Sequence 82, Appl
					Sequence 81, Appl
					Sequence 80, Appl
					Sequence 79, Appl
					Sequence 6, Appli

16	518.5	23.6	590	12	US-10-311-626-8	Sequence 8, Appli
17	507.5	23.1	295	9	US-09-764-870-364	Sequence 364, App
18	507.5	23.1	295	15	US-10-125-540-364	Sequence 364, App
19	447	20.3	413	11	US-09-778-418-24	Sequence 24, Appl
20	418	19.0	412	12	US-09-764-875-683	Sequence 683, App
21	395.5	18.0	373	12	US-09-764-875-770	Sequence 770, App
22	395.5	18.0	375	12	US-09-764-875-898	Sequence 898, App
23	344	15.6	199	12	US-09-764-875-771	Sequence 771, App
24	330	15.0	234	12	US-09-764-875-767	Sequence 767, App
25	330	15.0	267	9	US-09-764-870-359	Sequence 359, App
26	330	15.0	267	15	US-10-125-540-359	Sequence 359, App
27	321.5	14.6	671	12	US-10-311-626-5	Sequence 5, Appli
28	320.5	14.6	671	12	US-10-108-260A-2460	Sequence 2460, Ap
29	319.5	14.5	219	10	US-09-925-300-1448	Sequence 1448, Ap
30	301.5	13.7	555	12	US-10-104-047-2530	Sequence 2530, Ap
31	296.5	13.5	208	9	US-09-764-870-497	Sequence 497, App
32	296.5	13.5	208	12	US-09-764-875-1071	Sequence 1071, Ap
33	296.5	13.5	208	15	US-10-125-540-497	Sequence 497, App
34	254.5	11.6	501	15	US-10-177-233-447	Sequence 447, App
35	253	11.5	407	9	US-09-764-870-375	Sequence 375, App
36	253	11.5	407	15	US-10-125-540-375	Sequence 375, App
37	250	11.4	862	12	US-10-339-782-492	Sequence 492, App
38	250	11.4	910	15	US-10-177-233-449	Sequence 449, App
39	245	11.1	376	15	US-10-177-233-451	Sequence 451, App
40	238.5	10.8	203	12	US-10-029-386-34078	Sequence 34078, A
41	235.5	10.7	336	12	US-10-168-659-22	Sequence 22, Appl
42	235.5	10.7	348	9	US-09-764-870-502	Sequence 502, App
43	235.5	10.7	348	12	US-09-764-875-1068	Sequence 1068, Ap
44	235.5	10.7	348	15	US-10-125-540-502	Sequence 502, App
45	235	10.7	334	9	US-09-764-870-367	Sequence 367, App

ALIGNMENTS

RESULT 1

US-09-954-570-2
; Sequence 2, Application US/09954570
; Publication No. US20030033614A1
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Method for Identifying Horizontally Modulated Genes
; FILE REFERENCE: 267/116
; CURRENT APPLICATION NUMBER: US/09/954,570
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-570-2

Query Match 100.0%; Score 2201; DB 11; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAPITTSREDFEIPVTGGI	100.0%;	Score 2201;	DB 11;	Length 425;
Db	1	MAPITTSREDFEIPVTGGI	100.0%;	Pred. No. 1.3e-195;	Mismatches 0;	Indels 0;
Qy	61	DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDNLGNFPKTNLKPGSPSLEN	120			
Db	61	DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDNLGNFPKTNLKPGSPSLEN	120			
Qy	121	ATPKLFLGEGEKESVSPESLKSSTLSLTSSEKQKLGITLFFSLEYNFERKAFVYNKEARGL	180			
Db	121	ATPKLFLGEGEKESVSPESLKSSTLSLTSSEKQKLGITLFFSLEYNFERKAFVYNKEARGL	180			
Qy	181	PAMDQSMSTSDYIKWTLPEKKHKVTRVLRKTLDPAFDETFTFYGIPYQIOELAHFF	240			
Db	181	PAMDQSMSTSDYIKWTLPEKKHKVTRVLRKTLDPAFDETFTFYGIPYQIOELAHFF	240			


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; Sequence 1072, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1072
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (24)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-1072

Query Match          27.4%; Score 603; DB 12; Length 188;
Best Local Similarity 58.4%; Pred. No. 9.5e-48;
Matches 108; Conservative 41; Mismatches 34; Indels 2; Gaps 2;

QY 242 ILSEFRSDDDIIGEVLIPLSGIESEGKMLMREIIKRNVRKSSGRGELLISLCYQSTT 301
Db 3 VLSEFRFRDDDVIGEVVPLAXVDPSTGKVLTRDIIKRNIOKICISRGELQVLSYQFVA 62

QY 302 NTLTVVLKARHLPKSDVSGLS-DPVYKVNLYHAKKRISKKTTHVKKCTPNAVENELFVF 360
Db 63 QMTVVVLKARHLPKMDITGLSGNPPYKVNYYGRKRIAKKTHVKKCTLPNPFNESFIY 122

QY 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVLGA-AAEGTGGHEHKEICDYPRRQIAKW 419
Db 123 DIPTDLLPDISIEFLVIDFDRTTKNEVVGRLILGAHVSVTASGAEHWEVCESPRKPVAKW 182

QY 420 HVLCDD 424
Db 183 HSLSE 187

RESULT 7
US-10-125-540-368
; Sequence 368, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 368
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-125-540-368

Query Match          27.4%; Score 603; DB 15; Length 188;
Best Local Similarity 58.4%; Pred. No. 9.5e-48;
Matches 108; Conservative 41; Mismatches 34; Indels 2; Gaps 2;

QY 242 ILSEFRSDDDIIGEVLIPLSGIESEGKMLMREIIKRNVRKSSGRGELLISLCYQSTT 301
Db 3 VLSEFRFRDDDVIGEVVPLAXVDPSTGKVLTRDIIKRNIOKICISRGELQVLSYQFVA 62

QY 302 NTLTVVLKARHLPKSDVSGLS-DPVYKVNLYHAKKRISKKTTHVKKCTPNAVENELFVF 360
Db 63 QMTVVVLKARHLPKMDITGLSGNPPYKVNYYGRKRIAKKTHVKKCTLPNPFNESFIY 122

QY 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVLGA-AAEGTGGHEHKEICDYPRRQIAKW 419
Db 123 DIPTDLLPDISIEFLVIDFDRTTKNEVVGRLILGAHVSVTASGAEHWEVCESPRKPVAKW 182

QY 420 HVLCDD 424
Db 183 HSLSE 187

RESULT 8
US-09-764-870-365
; Sequence 365, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 365
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-365

Query Match          27.4%; Score 603; DB 9; Length 461;
Best Local Similarity 40.8%; Pred. No. 3.7e-47;
Matches 128; Conservative 62; Mismatches 104; Indels 20; Gaps 6;

QY 115 PSDLENATPKLFLEGEKESVPSLSKSTSLTSEEKQELGTLFFSLEYNPERKAFVYNI 174
Db 152 PTSIGRIKPELY--KQKSVGDGDAKS-----EATKSCGKINFSLRYDYETETLIVRI 201

QY 175 KEARGLUPAMDEQSMSTDPIYKMTILPEKHKHVTRVLRTLDPAFDDETFTFYGIPTQIQ 234
Db 202 LKAFDLPKADFQCG-SSDPYVKIYLLPDRKCKLQTRVHRKTLNPTFDENFHF-PVPYEELA 259

QY 235 ELAHEFTILSEDFRSDDDIIGEVLIPLSGIESEGKMLMREIIKRNVR-----KSSGRGE 290
Db 260 DRKLHLSVDFDRFSRHDIMGEVILD---NLFEASDLSETSIWKIOIYATSESDVLDGE 315

QY 291 LLTSLCYQSTTNTLTIVVLKARHLPKSDVSGLSGSDPYKVNLYHAKKRISKKTTHVKKCTP 350
Db 316 INFSLCYLPTAGRLTLTVTKCRNLKAMDITGYSDPYKVKVSLLCDGRRLKKKKTKIKKNIL 375
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QY 351 NAVNELVFDPICGLEDISVEFLVLDSEGRNEVIGQLVGLAAAGCTGGHWEICD 410
Db 376 NPVYNEAIIIFDIPENMDQVSLISVMDYDRVGHNEIIGVCRVGTAEGLGRDHWNEMLA 435
QY 411 YPRQRIAKWHVLC 424
Db 436 YPRKPIAHWSLVE 449

RESULT 9

US-10-125-540-365
; Sequence 365, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 365
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-365

Query Match 27.4%; Score 603; DB 15; Length 461;
Best Local Similarity 40.8%; Pred. No. 3.7e-47;
Matches 128; Conservative 62; Mismatches 104; Indels 20; Gaps 6;

QY 115 PSDLENATPKLFLGEEKESVSPESLKSSTSLTSEKQKGLTFLFSLEYNFERKAFVNI 174
Db 152 PTSGRIKPELY---KQKSVGDDEAKS-----EATKSCGKINFSLRYDYETETLIVRI 201
QY 175 KEARGLPAMDEQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPAPDETFYGIPTQIQ 234
Db 202 LKAFDLPKADFCG-SSDPYVKIYLLPDRCKLQTRVHRKTLNPTFDENPHF-PVPYEELA 259

QY 235 ELALHFTILSFDRSRDDIIGEVILPLSGIELSEGMNREIIRKNVR---KSSGRGE 290
Db 260 DRXLHLSVDFDRFSRDMIGEVLDD---NLFEASDLSTRETSIWKDIQVATSESDVLGE 315
QY 291 LLISLCYQSTNTILTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTP 350
Db 316 IMFSLCYLPTAGRLTLTVIKCRNLKAMDITGSDPYVKVSLLCDGRRLKCKTKTKNTL 375
QY 351 NAVNELVFDPICGLEDISVEFLVLDSEGRNEVIGQLVGLAAAGCTGGHWEICD 410
Db 376 NPVYNEAIIIFDIPENMDQVSLISVMDYDRVGHNEIIGVCRVGTAEGLGRDHWNEMLA 435

411 YPRQRIAKWHVLC 424

436 YPRKPIAHWSLVE 449

RESULT 10

US-10-231-913-82
; Sequence 82, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsbrook II, John P.

; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Beldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zehusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 82
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-231-913-82

Query Match 27.4%; Score 603; DB 12; Length 511;
Best Local Similarity 40.4%; Pred. No. 4.4e-47;
Matches 127; Conservative 64; Mismatches 103; Indels 20; Gaps 6;

QY 115 PSDLENATPKLFLGEEKESVSPESLKSSTSLTSEKQKGLTFLFSLEYNFERKAFVNI 174
Db 202 PTSGRIKPELY---KQKSVGDDEAKS-----EAAKSCGKINFSLRYDYSESTLIVRI 251
QY 175 KEARGLPAMDEQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPAPDETFYGIPTQIQ 234
Db 252 LKAFDLPKADFCG-SSDPYVKIYLLPDRCKLQTRVHRKTLNPTFDENPHF-PVPYEELA 309
QY 235 ELALHFTILSFDRSRDDIIGEVILPLSGIELSEGMNREIIRKNVR---KSSGRGE 290
Db 310 DRXLHLSVDFDRFSRDMIGEVLDD---NLFEASDLSTRETSIWKDIQVATSESDVLGE 365

QY 291 LLISLCYQSTNTILTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTP 350
Db 366 IMFSLCYLPTAGRLTLTVIKCRNLKAMDITGSDPYVKVSLLCDGRRLKCKTKTKNTL 425
QY 351 NAVNELVFDPICGLEDISVEFLVLDSEGRNEVIGQLVGLAAAGCTGGHWEICD 410
Db 426 NPVYNEAIIIFDIPENMDQVSLISVMDYDRVGHNEIIGVCRVGTAEGLGRDHWNEMLA 485
QY 411 YPRQRIAKWHVLC 424
Db 486 YPRKPIAHWSLVE 499

RESULT 11

US-10-231-913-81
; Sequence 81, Application US/10231913
; Publication No. US20040005576A1

; GENERAL INFORMATION:
 ; APPLICANT: Guo, Xiaojia S.
 ; APPLICANT: Li, Li
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Vernet, Corine A.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Alsobrook II, John P.
 ; APPLICANT: Edinger, Schlomit
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Boldog, Ference L.
 ; APPLICANT: Colman, Steven D.
 ; APPLICANT: Eisen, Andrew J.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Zehusen, Bryan D.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-216
 ; CURRENT APPLICATION NUMBER: US/10/231,913
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: 60/251,660
 ; PRIOR FILING DATE: 2000-12-06
 ; PRIOR APPLICATION NUMBER: 60/255,029
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: 60/260,326
 ; PRIOR FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 60/263,800
 ; PRIOR FILING DATE: 2001-01-24
 ; PRIOR APPLICATION NUMBER: 60/269,942
 ; PRIOR FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 60/286,183
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: 60/313,627
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/318,712
 ; NUMBER OF SEQ ID NOS: 292
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 81
 ; LENGTH: 511
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-231-913-81

Query Match 27.2%; Score 598; DB 12; Length 511;
 Best Local Similarity 40.4%; Pred. No. 1.3e-46;
 Matches 127; Conservative 63; Mismatches 104; Indels 20; Gaps 6;
 QY 115 PSDLENATPKLFLGEKEKSVSPESLSTLSTSEKQKGLFLPSLYNFKKAFVMI 174
 Db 202 PISGRIKPELY---KQKSVDDDAK-----EAAKSCGKINFSLRYDSESLIVRI 251
 QY 175 KEARGLPAMDFQSMSTDPIYKMTILPEKKGKVKTVLRKTLDPARDETTFYGIPTQIQ 234
 Db 252 LKAPDLPAKDFCG-SSDPYVKIYLLPDRCKLQTRVHRKTLNPTFDENFHF-PVPYEELA 309
 QY 235 ELALHFTILSDFRSRDILIGELVPLSGIEUSEGMLNREILIKENVR---KSSGRGE 290
 Db 310 DRKLHLSVDFDRSRHMGIEVLDD----NLFASDLSETSIWKDIQIATSESVDLGE 365
 QY 291 LLSLCYQSTNTLTITVVLVYKARHLPKSDVSLSDPYVKVNLVYHAKKRISKKTHVKCTP 350
 Db 366 IMFSLCYLPTAGRLTLTVIKCNLKAMDTGSDPYVKVSLCDGRLAKKTKTINKNTL 425
 QY 351 NAVNELVFVPIPCGLEDISVEFLVLDSEGRSNEVIGQLVLGAAAGTGGEHWKEICD 410

Db 426 NPVYNEAIFDIPPENMDQVSLISVMDYDRVGHNEIIGVCRVGINAEGIGRDHWEMLA 485
 QY 411 YPRRQIAKWHVLC D 424
 Db 486 YPRKPIAHWSLIVE 499
 RESULT 12
 US-10-231-913-80
 ; Sequence 80, Application US/10231913
 ; Publication No. US20040005576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo, Xiaojia S.
 ; APPLICANT: Li, Li
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Vernet, Corine A.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Alsobrook II, John P.
 ; APPLICANT: Edinger, Schlomit
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Boldog, Ference L.
 ; APPLICANT: Colman, Steven D.
 ; APPLICANT: Eisen, Andrew J.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Zehusen, Bryan D.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-216
 ; CURRENT APPLICATION NUMBER: US/10/231,913
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: 60/251,660
 ; PRIOR FILING DATE: 2000-12-06
 ; PRIOR APPLICATION NUMBER: 60/255,029
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: 60/260,326
 ; PRIOR FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 60/263,800
 ; PRIOR FILING DATE: 2001-01-24
 ; PRIOR APPLICATION NUMBER: 60/269,942
 ; PRIOR FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 60/286,183
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: 60/313,627
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/318,712
 ; NUMBER OF SEQ ID NOS: 292
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 80
 ; LENGTH: 498
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-231-913-80

Query Match 26.9%; Score 592; DB 12; Length 498;
 Best Local Similarity 34.6%; Pred. No. 4.4e-46;
 Matches 158; Conservative 72; Mismatches 156; Indels 70; Gaps 16;
 QY 20 IFSAFGL-VFTVSLFA-WICQQRSSKNKTPYKFKVHLKGVDIYPENLNS--KKKFGA 75
 Db 60 VVSCFGLALLVVSFLVFWKLC-----WPCWKSCLVAPNVSTLPQSISSAPTEVFET 110
 QY 76 DDKNEV-KNKPAVPKNSLHLDLEKRDINGNFP---KTNLK-----FGSPS 116

111 EKKKEVEENKPAK-AIEPAIKISHTSPDIPAEVQTALKKEHLKHARVQRTDPTSS 169
117 -----DLENATPKLFLGEEKES-----VSPESLKSSTSTSE-----EK 150
170 RHNSFRHLPRQMNVSDFSMGTEPVLRGETRTSIRIKPELYKQK-SVDSEGNRKDD 228
151 QKIGTLFFSLEYNEFKAFVNNIKERGLPAMDEQSMSTDPYIKMTILPEKKHKVTRV 210
229 VTCGKLNLFALQDYENELLVVKIIRKALDLPKADSTG-TSDPYVKIYLLPRKKKFQTRV 287
211 LRKTLDPAPDETFYGIPTQIOELALHFTILSDFRSRDDIIGEVLIPLSGIELSGK 270
288 HRKTLNPLFDELQF-PVVDQLSNRKLHRSIYDFRFRSHDMIGEVLID-----NLFEVS 342
271 MLMNREIKRNV-----KSSGRGELLISLCYQSTNTLTVVVLKARHLPKSDVSGLSDPY 326
343 DLSREATVWKDIHCATTESDMLGEIMFSLCYLPTAGRWTLTVKRCNLKAMDITGSSDPY 402
327 VKVNLHYAKRISKKTHVKCTPNAVNELFVDPIDCEGLEDISVEFLVLDSEGRSNE 386
403 KVSMLCEGRLLKRRKTTTKNTLNPVYNEAIIFDIPPENVDQVSLCIAVMDYDRVGNE 462
387 VIGQLVGLAAAGTGGHMKKEICDYPRIQAKHVL 422
463 VIGVCTGLDAEGLGRDHNMELAYHRKEPITHWHPL 498

RESULT 13

US-10-231-913-79

; Sequence 79, Application US/10231913

; Publication No. US20040005576A1

; GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia S.

; APPLICANT: Li, Li

; APPLICANT: Patturajan, Meera

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Vernet, Corine A.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Edinger, Schlomit

; APPLICANT: Peyman, John A.

; APPLICANT: Stone, David J.

; APPLICANT: Ellerman, Karen

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Boldog, Ference L.

; APPLICANT: Colman, Steven D.

; APPLICANT: Eisen, Andrew J.

; APPLICANT: Liu, Xiaohong

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-216

; CURRENT APPLICATION NUMBER: US/10/231,913

; CURRENT FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: 60/251,660

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: 60/255,029

; PRIOR FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: 60/260,326

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/263,800

; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: 60/269,942

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/286,183

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: 60/313,627

; PRIOR FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: 60/251,660

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: 60/255,029

; PRIOR FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: 60/260,326

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/263,800

; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: 60/269,942

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/286,183

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: 60/313,627

; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-231-913-79

Query Match 26.8%; Score 590; DB 12; Length 523;
Best Local Similarity 33.7%; Pred. No. 7.3e-46;
Matches 154; Conservative 74; Mismatches 161; Indels 68; Gaps 14;

QY 20 IFSAFGL-VFTVSLFA-WICQKSSKNKTPPVYKVFVHLKGVDIYPENLNS--KKKFGA 75
Db 60 VVSFCGLALLVSLFVFWKLC-----WPCWKSCLVAPNLVSLVQSISSAPTEVFET 110
QY 76 DDKNEVKN-----KPAVPKNSLHDL-----EKRDINGNFPKTNLKPQSPS- 116
Db 111 EEKKEVEENKPAKPAKATEPAIKISHTSPDIPAEVQTALKKEHLKHARVQRTTEPTSSR 170
QY 117 -----DLENATPKLFLGEEKES-----VSPESLKSSTSTSE-----EKQ 151
Db 171 HNSFRHLPRQMNVSDFSVGTETPILQRTSIRIKPELYKQK-SVDSEGNRKDDV 229
QY 152 EKLGTLLFFSLEYNEFKAFVNNIKERGLPAMDEQSMSTDPYIKMTILPEKKHKVTRVL 211
Db 230 KTCGKLNLFALQDYENELLVVKIIRKALDLPKADSTG-TSDPYVKIYLLPRKKKFQTRV 288
QY 212 RKTLDPAFDETFYGIPTQIOELALHFTILSDFRSRDDIIGEVLIPLSGIELSEGM 271
Db 289 RKTNLPLFDELQF-PVVDQLSNRKLHRSIYDFRFRSHDMIGEVLID-----NLFEVS 343
QY 272 LMNREIKRNV-----KSSGRGELLISLCYQSTNTLTVVVLKARHLPKSDVSGLSDPY 327
Db 344 LSREATVWKDIHCATTESDMLGEIMFSLCYLPTAGRWTLTVKRCNLKAMDITGSSDPY 403
QY 328 KVNLYHAKRISKKTHVKCTPNAVNELFVDPIDCEGLEDISVEFLVLDSEGRSNEV 387
Db 404 KVSMLCEGRLLKRRKTTTKNTLNPVYNEAIIFDIPPENVDQVSLCIAVMDYDRVGNEV 463
QY 388 IGQLVGLAAAGTGGHMKKEICDYPRIQAKHVLCD 424
Db 464 VIGVCTGLDAEGLGRDHNMELAYHRKEPITHWHPLLE 500

RESULT 14

US-10-231-913-78

; Sequence 78, Application US/10231913

; Publication No. US20040005576A1

; GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia S.

; APPLICANT: Li, Li

; APPLICANT: Patturajan, Meera

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Vernet, Corine A.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Edinger, Schlomit

; APPLICANT: Peyman, John A.

; APPLICANT: Stone, David J.

; APPLICANT: Ellerman, Karen

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Boldog, Ference L.

; APPLICANT: Colman, Steven D.

; APPLICANT: Eisen, Andrew J.

; APPLICANT: Liu, Xiaohong

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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:11:55 ; Search time 21 Seconds
(without alignments)
856.291 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201
Sequence: 1 MAPTTTGREPDEIPTVVGI.....KEICDPRQIAKWHVLCDS 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2201	100.0	425	3	US-09-036-315-2
2	2006	91.1	425	3	US-09-036-315-5
3	605	27.5	121	3	US-09-036-315-7
4	581	26.4	422	3	US-08-872-979-8
5	577	26.2	113	3	US-09-036-315-10
6	361.5	16.4	355	3	US-08-872-979-7
7	338.5	15.4	375	3	US-08-872-979-3
8	310	14.1	60	3	US-09-036-315-24
9	288	13.1	138	2	US-08-609-049A-17
10	288	13.1	138	3	US-09-170-996-17
11	271	12.3	120	3	US-09-036-315-9
12	244	11.1	115	3	US-09-036-315-8
13	226	10.3	46	3	US-09-036-315-25
14	182.5	8.3	140	2	US-08-609-049A-16
15	182.5	8.3	140	3	US-09-170-996-16
16	182	8.3	95	4	US-09-800-971-10
17	180	8.2	34	3	US-09-036-315-22
18	169	7.7	33	3	US-09-036-315-26
19	166	7.5	31	3	US-09-036-315-21
20	158	7.2	916	4	US-09-417-197-73
21	158	7.2	1658	4	US-08-609-049A-13
22	158	7.2	1658	3	US-09-170-996-13
23	158	7.2	1726	2	US-08-609-049A-30
24	158	7.2	1726	3	US-09-170-996-30
25	157.5	7.2	136	2	US-08-609-049A-18
26	157.5	7.2	136	3	US-09-170-996-18
27	155.5	7.1	117	3	US-09-036-315-6

28 152.5 6.9 1876 2 US-08-609-049A-12 Sequence 12, Appl
29 152.5 6.9 1876 3 US-09-170-996-12 Sequence 12, Appl
30 149.5 6.8 137 2 US-08-609-049A-14 Sequence 14, Appl
31 149.5 6.8 137 3 US-09-170-996-14 Sequence 14, Appl
32 144.5 6.6 1876 2 US-08-609-049A-28 Sequence 28, Appl
33 144.5 6.6 1876 3 US-09-170-996-28 Sequence 28, Appl
34 144 6.5 1686 4 US-09-355-160D-2 Sequence 2, Appl
35 141 6.4 671 6 5266464 Patent No. 5266464
36 136 6.2 804 3 US-08-909-954-2 Sequence 2, Appl
37 131.5 6.0 799 3 US-08-909-954-4 Sequence 4, Appl
38 129.5 5.9 137 2 US-08-609-049A-15 Sequence 15, Appl
39 129.5 5.9 137 3 US-09-170-996-15 Sequence 15, Appl
40 125 5.7 25 3 US-09-036-315-23 Sequence 23, Appl
41 117 5.3 40 4 US-09-023-905A-31 Sequence 31, Appl
42 117 5.3 927 3 US-08-895-601-6 Sequence 6, Appl
43 109 5.0 990 2 US-08-392-625-20 Sequence 20, Appl
44 109 5.0 990 2 US-08-466-961A-20 Sequence 20, Appl
45 102.5 4.7 990 2 US-08-645-193B-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-036-315-2 ; Sequence 2, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-036-315-2

Query Match 100.0%; Score 2201; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 9.6e-217;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAPITTSREDFBIPTVVGIFSAFGLVFTVSLFAMICCOCKSSKNTKPPYKVFVHLKGV 60
Db 1 MAPITTSREDFBIPTVVGIFSAFGLVFTVSLFAMICCOCKSSKNTKPPYKVFVHLKGV 60
QY 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
Db 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
QY 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNPERKAFVNNIKEARGL 180
Db 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNPERKAFVNNIKEARGL 180
QY 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLPADFETFTFYGIPYTOIQELALHF 240
Db 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLPADFETFTFYGIPYTOIQELALHF 240
QY 241 TILSFDRFSRDDIIGEVLIPLSGIELSEGMMLNREIIKRNVRKSSGRGELLISLCYQST 300
Db 241 TILSFDRFSRDDIIGEVLIPLSGIELSEGMMLNREIIKRNVRKSSGRGELLISLCYQST 300
QY 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKKCTPNVAFNELFVF 360
Db 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKKCTPNVAFNELFVF 360
QY 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVGAAGTGGEHWKEICDYPRQIAKWH 420
Db 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVGAAGTGGEHWKEICDYPRQIAKWH 420
QY 421 VLCDG 425
Db 421 VLCDG 425
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RESULT 2

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US-09-036-315-5
; Sequence 5, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
```

```
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..425
; OTHER INFORMATION: /note= "rat synaptotagmin 4 (SYT4)"
US-09-036-315-5
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Query Match 91.1%; Score 2006; DB 3; Length 425;
Best Local Similarity 89.9%; Pred. No. 8,9e-197;
Matches 382; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAPITTSREDFBIPTVVGIFSAFGLVFTVSLFAMICCOCKSSKNTKPPYKVFVHLKGV 60
Db 1 MAPITTSREDFBIPTVVGIFSAFGLVFTVSLFAMICCOCKSSKNTKPPYKVFVHLKGV 60
QY 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
Db 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
QY 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNPERKAFVNNIKEARGL 180
Db 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNPERKAFVNNIKEARGL 180
QY 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLPADFETFTFYGIPYTOIQELALHF 240
Db 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLPADFETFTFYGIPYTOIQELALHF 240
QY 241 TILSFDRFSRDDIIGEVLIPLSGIELSEGMMLNREIIKRNVRKSSGRGELLISLCYQST 300
Db 241 TILSFDRFSRDDIIGEVLIPLSGIELSEGMMLNREIIKRNVRKSSGRGELLISLCYQST 300
QY 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKKCTPNVAFNELFVF 360
Db 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKKCTPNVAFNELFVF 360
QY 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVGAAGTGGEHWKEICDYPRQIAKWH 420
Db 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVGAAGTGGEHWKEICDYPRQIAKWH 420
QY 421 VLCDG 425
Db 421 VLCDG 425
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RESULT 3

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US-09-036-315-7
; Sequence 7, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/036,315
 FILING DATE: 06-MAR-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/047,811
 FILING DATE: 15-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/041,246
 FILING DATE: 07-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 REFERENCE/DOCKET NUMBER: 018002-000210US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 121 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..121
 OTHER INFORMATION: /note= "Repro-PC-1.0 (PC-20) "B"
 OTHER INFORMATION: internal repeat (amino acid
 OTHER INFORMATION: positions 276-397)"

US-09-036-315-7

Query Match 27.5%; Score 605; DB 3; Length 121;
 Best Local Similarity 99.2%; Pred. No. 3.5e-54;
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

276 EIKRNVKSSRGELLISLCYQSTTNTLTVVVKARHLPKSDVSLSDPYVKNLYHAK 335
 1 EIKRNVKSSRGELLISLCYQSTTNTLTVVVKARHLPKSDVSLSDPYVKNLYHAK 60

336 KRISKKTHVKCTPNVAVNELFVDFDIPCEGLEDSVFLVLDSEGRSNEVIGQLVGA 395
 61 KRISKKTHVKCTPNVAVNELFVDFDIPCEGLEDSVFLVLDSEGRSNEVIGQLVGA 120

396 A 396
 121 A 121

RESULT 4

US-08-872-979-8
 Sequence 8, Application US/08872979
 Patent No. 6074844

GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Lal, Preeti
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/872,979
 FILING DATE: Herewith

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0320 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 422 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 338658
 US-08-872-979-8

Query Match 26.4%; Score 581; DB 3; Length 422;

Best Local Similarity 39.9%; Pred. No. 7.5e-51;

Matches 132; Conservative 65; Mismatches 114; Indels 20; Gaps 8;

105 FPKTNLKPSPDLNATPKLFLGEEKESVSPESLK---SSTSLT-SEEK-----QEKLG 155
 85 FKKNKKKKEKGGKNAIMKVDKGLTKMDQALKDDDAETGLTDGEEKKEPEKEKLG 144

156 TLFFSLVYNERKAFVNIKEARGLPAMDEQSMSTDPYIKMTILPEKHKVKTIVLRKTL 215
 145 KLVSLDYDFQNNQLLVGLIQAAELPALD-MGTSDPYVKKVFLPLDPKKKFKFKVIRKTL 203

216 DPAPDETFTYIGIPYQIQELALHFTILSFDRFSRDDIIGEVLLIPUSGIEL-----SEGKM 271
 204 NPVNEQFTF-KVPYSELGGKTLWAVYDFDRFSKHDIIIGEFKVPMTVDVFGHVTEWRD 262

272 LMREIIRNVKSSRGELLISLCYQSTTNTLTVVVKARHLPKSDVSLSDPYVKNL 331
 263 LQSAE--KEQEK--LGDICFSLRYVPTAGKLTVVILEAKNLKMDVGLSDPYVVKIHL 317

332 YHAKRISKTHVKCTPNVAVNELFVDFDIPCEGLEDSVFLVLDSEGRSNEVIGOL 391
 318 MONGKRLKKKTKTKNTLNPYNESFSEFVEPFIQKVQVVVTVLDYDKIGKNDATGKV 377

392 VLGAAGTGGEGHWEKICDYPRRQIAKWHVL 422
 378 FVGYNSTGAELRHWSMDLANPRPPIAQWHTL 408

RESULT 5

US-09-036-315-10
 Sequence 10, Application US/09036315
 Patent No. 6218523
 GENERAL INFORMATION:
 APPLICANT: French, Cynthia K.
 APPLICANT: Schneider, Patrick A.
 APPLICANT: Yamamoto, Karen K.
 TITLE OF INVENTION: Prostate Cancer-Specific Marker
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Stozella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "Repro-PC-1.0 (PC-20) "A"
; OTHER INFORMATION: internal repeat (amino acid
; OTHER INFORMATION: positions 150-263)"
; US-09-036-315-10

Query Match 26.2%; Score 577; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 KOEKLGTILFFSLEYNFERKAFVNIKEARGLPAMDEQSMTPYIKMTILPEKKHKVKTR 209
Db 1 KOEKLGTILFFSLEYNFERKAFVNIKEARGLPAMDEQSMTPYIKMTILPEKKHKVKTR 60

QY 210 VLKTLDPAPDETFTFYGIPYQIOELALHFTILSDFRSDDIIGEVLIPLS 262
Db 61 VLKTLDPAPDETFTFYGIPYQIOELALHFTILSDFRSDDIIGEVLIPLS 113

RESULT 6
US-08-872-979-7
; Sequence 7, Application US/08872979
; Patent No. 6074844
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,979
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0320 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 643658
; US-08-872-979-7

Query Match 16.4%; Score 361.5; DB 3; Length 355;
Best Local Similarity 30.2%; Pred. No. 1.7e-28;
Matches 94; Conservative 62; Mismatches 120; Indels 35; Gaps 6;

QY 130 EKESVPESILKSTSLTSEEK-----QEKLGTLFFSLEYNFERKAFVNIKEAR 178
Db 39 DKETVGLGSARNSTTHLVQPDVDCLEPCSGDQOQWGRLLLSLEYDFGSGQEIIVGLQAG 98

QY 179 GLPAMDEQSMTPYIKMTILPEKKHKVKTRVLKTLDPAPDETFTFYGIPYQIOELAL 238
Db 99 NLKA---EGTADPYAWVSQSGRRHETKVRHGTLSPMFEETCCFL-VPPAELPKATL 153

QY 239 HFTILSDFRSDDIIGEVLIPLSGLIELSEGNLMNREIKR-----NVRKSSGRGEL 291
Db 154 KVLQWDFKRFSEHEPLGELQLPLGTVDL-----QHVLESWYQLGPPGTTEPEQMDEL 205

QY 292 LISLCYQSTTNLTVVVLKARHLKSDVSGLSDPYVKNLYHAKKRISKKKTHVKKCTPN 351
Db 206 CFSRLYFVSSGLTQVVVLEARGLN----PGLAEAYVKIQMLNQRKWKSKTSKKGTTT 261

QY 352 AVFNELFVDFIPCEGLEDISVEFLVDSRGRNEVIGQLVGLAAAGTGEHWEKICDY 411
Db 262 PYFNEAFVLPVSQVQLQSDVLVLAVWARGQLRTEPVGKVLGSRASGQPLQHWADMLAH 321

QY 412 PRQIAKWHVL 422
Db 322 ARRPQAQWHHL 332

RESULT 7
US-08-872-979-3
; Sequence 3, Application US/08872979
; Patent No. 6074844
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,979
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,246
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-000210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-315-24

Query Match          14.1%   Score 310;   DB 3;   Length 60;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 199 LPBKHKVKTRVLKTLDPADFETFTYGIPYTOIQELALHFTILSFDRSRDDIIGVL 258
DB 1 LPBKHKVKTRVLKTLDPADFETFTYGIPYTOIQELALHFTILSFDRSRDDIIGVL 60

RESULT 9
US-08-609-049A-17
Sequence 17, Application US/08609049A
Patent No. 5948664
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A
FILING DATE: 29-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:

```

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; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-049A-17
Query Match 13.1%; Score 288; DB 2; Length 138;
Best Local Similarity 46.8%; Pred. No. 1.3e-21;
Matches 59; Conservative 22; Mismatches 45; Indels 0; Gaps 0;

QY 289 GELLISLCYQSTNTNLTVVVLKARHLPKSDVSGLSDPYVKVNLHYHAKKRISKKTHVKKC 348
Db 12 GDICTSLRYVPTAGKLTVCILLEAKNLKMDVSGLSDPYVKVNLHYHAKKRISKKTHVKKC 71

QY 349 TPNVAFNELFVFDIPCEGLDISEVFLVLDSESGSNEVIGQLVLAAGTGEHWEI 408
Db 72 TLNPFNFESFSEIPFEIQKQVQVVTVLDYDKLGKNEAIGKIFVGSNATGTLRHWSDM 131

QY 409 CDYPRR 414
Db 132 LANPRR 137

RESULT 10
US-09-170-996-17
; Sequence 17, Application US/09170996
; Patent No. 6291220
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Molz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,996
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,049
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-170-996-17
Query Match 13.1%; Score 288; DB 3; Length 138;
Best Local Similarity 46.8%; Pred. No. 1.3e-21;
Matches 59; Conservative 22; Mismatches 45; Indels 0; Gaps 0;

QY 289 GELLISLCYQSTNTNLTVVVLKARHLPKSDVSGLSDPYVKVNLHYHAKKRISKKTHVKKC 348
Db 12 GDICTSLRYVPTAGKLTVCILLEAKNLKMDVSGLSDPYVKVNLHYHAKKRISKKTHVKKC 71

QY 349 TPNVAFNELFVFDIPCEGLDISEVFLVLDSESGSNEVIGQLVLAAGTGEHWEI 408
Db 72 TLNPFNFESFSEIPFEIQKQVQVVTVLDYDKLGKNEAIGKIFVGSNATGTLRHWSDM 131

QY 409 CDYPRR 414
Db 132 LANPRR 137

RESULT 11
US-09-036-315-9
; Sequence 9, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..120
; OTHER INFORMATION: /note= "synaptotagmin "A" internal
; OTHER INFORMATION: repeat (amino acid positions 134-254) "
US-09-036-315-9
Query Match 12.3%; Score 271; DB 3; Length 120;
Best Local Similarity 45.3%; Pred. No. 5.5e-20;
Matches 53; Conservative 29; Mismatches 33; Indels 2; Gaps 2;

QY 149 EQEKLGTILFFSILEYNERKAFVNTKEARGLPAMDEQSWTSDEYIKMTILPEKKGKVKYKT 208
Db 5 KEEELKGLQYSLDYDFQNNQLVIGIQAELPALD-MGGTSDPYVKVFLPLPKKKKPEF 63
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RESULT 13

RESULT 13

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609,049A
; APPLICATION NUMBER: US/08/609,049A
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-049A-16

Query Match      8.3%; Score 182.5; DB 2; Length 140;
Best Local Similarity 32.8%; Pred No. 8.2e-11;
Matches 39; Conservative 29; Mismatches 48; Indels 3; Gaps 2;

QY 154 LGTLFFSLYENFERKAFVYVNIKEARGLPAMDQSMSTSDPIYKMTILP--EKKHKVKTIVL 211
Db 11 LGALEFSLLYDQDSSSLHCTTIKAKGLKPMDSNGL-ADPYVKLHLPLGASKSKNKLRTKTL 69

QY 212 RKTLDPADEFTFYGIPTQIOELALHFTIILSFDRFSRDDIIGEVLLPLSGIELSEK 270
Db 70 RNTRNPIWNETLVYHGITDEDMQKTLRISVCDKDFGHNFEIGETFRFSKLKLPNQK 128

Search completed: February 20, 2004, 13:15:17
Job time : 22 secs

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609,049A
; APPLICATION NUMBER: US/08/609,049A
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-049A-16

Query Match      8.3%; Score 182.5; DB 2; Length 140;
Best Local Similarity 32.8%; Pred No. 8.2e-11;
Matches 39; Conservative 29; Mismatches 48; Indels 3; Gaps 2;

QY 154 LGTLFFSLYENFERKAFVYVNIKEARGLPAMDQSMSTSDPIYKMTILP--EKKHKVKTIVL 211
Db 11 LGALEFSLLYDQDSSSLHCTTIKAKGLKPMDSNGL-ADPYVKLHLPLGASKSKNKLRTKTL 69

QY 212 RKTLDPADEFTFYGIPTQIOELALHFTIILSFDRFSRDDIIGEVLLPLSGIELSEK 270
Db 70 RNTRNPIWNETLVYHGITDEDMQKTLRISVCDKDFGHNFEIGETFRFSKLKLPNQK 128

RESULT 15
US-09-170-996-16
; Sequence 16, Application US/09170996
; Patent No. 6291220
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Molz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,996
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,049
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:06:49 ; Search time 46 Seconds
(without alignments)
1466.496 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREDFEIPVTGVI.....KEICDYPQRQIAKMHVLCQG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2201	100.0	425	19 AAW74584	Repro-PC-1.0 prost
2	2201	100.0	425	19 AAW75782	Hormone-regulated
3	1162	52.8	431	22 AAW93420	Human polypeptide,
4	1162	52.8	431	22 AAW39577	Human polypeptide
5	1162	52.8	431	22 AAE17500	Human secretion an
6	1159	52.7	431	22 AAB92921	Human protein sequ
7	1154	52.4	486	22 AAM41363	Human polypeptide
8	757	34.4	474	22 ABB59179	Drosophila melanog
9	622.5	28.3	403	23 ABG70275	Human Synaptotagmi

10	622.5	28.3	474	22	ABB59660	Drosophila melanog
11	614	27.9	195	22	AAU87254	Novel central nerv
12	609	27.7	418	23	ABP69320	Human polypeptide
13	609	27.7	523	23	ABJ04645	Protein of NCVX 6
14	609	27.7	533	23	AAO19183	Human neurotransmi
15	607.5	27.6	1295	22	ABG0581	Novel human diagno
16	603.5	27.4	422	17	AAU87722	Mouse inositol pol
17	603	27.4	188	22	AAU87554	Novel central nerv
18	603	27.4	188	22	AAU19718	Human novel extrac
19	603	27.4	188	22	ABP47938	Human polypeptide
20	603	27.4	425	23	ABP69319	Human polypeptide
21	603	27.4	461	22	AAU19715	Human novel extrac
22	603	27.4	461	23	ABP47935	Human polypeptide
23	586.5	26.6	280	22	ABB59077	Drosophila melanog
24	581	26.4	906	23	ABB08635	GFP fusion protein
25	571.5	26.0	371	23	ABG70274	Human Synaptotagmi
26	568.5	25.8	389	23	ABB97511	Novel human protei
27	518.5	23.6	590	23	ABB05693	Human cell signal
28	518.5	23.6	590	23	AAE17499	Human secretion an
29	507.5	23.1	295	22	AAU19714	Human novel extrac
30	507.5	23.1	295	23	ABP47934	Human polypeptide
31	464.5	21.1	474	21	AAAB41973	Human polypeptide
32	464.5	21.1	474	22	AAAM40253	Human polypeptide
33	464.5	21.1	507	22	AAAM42039	Human polypeptide
34	447	20.3	413	24	ABR39434	Human GENSET polyp
35	428	19.4	412	18	AAW25032	Human Doc2-beta co
36	418	19.0	412	22	AAU87165	Novel central nerv
37	408	18.5	704	15	AAAS7421	Rabphilin-3A. Hom
38	405.5	18.4	361	23	ABU65212	Human NOVI25a prot
39	405.5	18.4	361	23	ABU65213	Human NOVI25a prot
40	395.5	18.0	373	22	AAU87252	Novel central nerv
41	395.5	18.0	375	22	AAU87380	Novel central nerv
42	393.5	17.9	405	20	AAU27275	Mouse Doc2alpha pr
43	384.5	17.5	400	17	AAW01114	Brain-specific pro
44	384.5	17.5	400	20	AAW83429	Human Doc2-alpha.
45	383	17.4	602	22	ABB71195	Drosophila melanog

ALIGNMENTS

RESULT 1

AAW74584

ID AAW74584 standard; Protein; 425 AA.

AC AAW74584;

XX

XX

DT 11-JAN-1999 (first entry)

XX

DE Repro-PC-1.0 prostate cancer-specific marker.

XX

KW Repro-PC-1.0; prostate cancer; marker; synaptotagmin; human;

KW diagnosis; vaccine; therapy.

XX

OS Homo sapiens.

XX

PN WC9839447-A1.

XX

PD 11-SEP-1998.

XX

XX

PF 06-MAR-1998; 98WO-US04488.

XX

PR 15-MAY-1997; 97US-0047811.

PR 07-MAR-1997; 97US-0041246.

XX

XX (REPR-) REPROGEN INC.

XX

PI French CK, Schneider PA, Yamamoto KK;

XX

DR WPI; 1998-506363/43.

DR N-PSDB; AAV54208.

XX

PT New isolated Repro-PC-1.0 polynucleotide(s) - are used to develop

PT products for the detection and prophylactic and therapeutic
 FT treatment of prostate cancer
 XX
 PS Claim 1; Page 68-69; 87pp; English.
 XX
 CC Repro-PC-1.0 is a novel prostate cancer-specific marker, which
 CC represents a novel human brain synaptotagmin isoform that may
 CC function in exocytosis and endocytosis pathways. Its amino acid
 CC sequence was deduced from cDNA clones (see AAV54208) isolated from
 CC a male LNCaP tumour cDNA library. The invention provides
 CC Repro-PC-1.0 polypeptides, fragments and immunogenic peptides
 CC (see also AAW30693-98) capable of inducing a Class I MHC-restricted
 CC cytotoxic T-lymphocyte response or a Class II MHC-restricted
 CC immune response against cells expressing Repro-PC-1.0. Also
 CC claimed are Repro-PC-1.0 polypeptide analogues that act as decoys,
 CC antibodies specific for Repro-PC-1.0, and methods for detecting
 CC Repro-PC-1.0 polypeptide in a sample, for diagnosis of prostate
 CC cancer (by detecting Repro-PC-1.0 mRNA or polypeptide in a sample),
 CC for detecting prostate cancer cells (e.g. using the antibodies of
 CC the invention), for following the progress of prostate cancer, for
 CC treatment of prostate cancer (e.g. using a Repro-PC-1.0 decoy
 CC polypeptide), and a polypeptide vaccine for eliciting an immune
 CC response against Repro-PC-1.0.
 XX
 SQ Sequence 425 AA;

Query Match 100.0%; Score 2201; DB 19; Length 425;
 Best Local Similarity 100.0%; Pred. No. 5.2e-196;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPYKFFVHLKGV 60
 DB 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPYKFFVHLKGV 60
 QY 61 DIYPENLNSKKKFGADDKNEVKKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 DB 61 DIYPENLNSKKKFGADDKNEVKKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 QY 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNERKAFVNNIKEARGL 180
 DB 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNERKAFVNNIKEARGL 180
 QY 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240
 DB 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240
 QY 241 TILSPDRSRDDIIGEVLIPLSGIELSEGMNREIKNVRKSGRGELLISLCYQST 300
 DB 241 TILSPDRSRDDIIGEVLIPLSGIELSEGMNREIKNVRKSGRGELLISLCYQST 300
 QY 301 TNLTVVVLKARHLPKSDVSGLSDPVVKVNLVYAKKRIKKKTHVKKCTPNAVFNELVF 360
 DB 301 TNLTVVVLKARHLPKSDVSGLSDPVVKVNLVYAKKRIKKKTHVKKCTPNAVFNELVF 360
 QY 361 DIPCEGLEDISVEFLVLDSEGRNREIVIGQLVLAAGGEGHWEICDYPRQIAKWH 420
 DB 361 DIPCEGLEDISVEFLVLDSEGRNREIVIGQLVLAAGGEGHWEICDYPRQIAKWH 420
 QY 421 VLCDG 425
 DB 421 VLCDG 425

RESULT 2
 AAW5782
 ID AAW5782 standard; Protein; 425 AA.
 XX
 AC AAW5782;

DT 21-DEC-1998 (first entry)
 DE Hormone-regulated Repro-PC-1.0 polypeptide.
 XX

KW Repro-PC-1.0; prostate cancer; LNCaP; hormone-regulated gene;
 XX human; synaptotagmin.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Region 150..252
 FT /note="repeat region"
 FT Region 276..396
 FT /note="repeat region"
 FT Domain 15..37
 FT /note="putative transmembrane domain"
 XX
 PN WO9839861-A1.
 XX
 PD 11-SEP-1998.
 XX
 PF 06-MAR-1998; 98WO-US04519.
 XX
 PR 15-MAY-1997; 97US-0047811.
 PR 07-MAR-1997; 97US-0041246.
 XX
 PA (REPR-) REPROGEN INC.
 XX
 PI French CK, Yamamoto KK;
 XX
 DR WPI; 1998-506379/43.
 DR N-PSDB; AAV57327.
 XX
 FT Identification of hormone-regulated traits, e.g. in cancers - by
 PT exposing grafts of biological material to different hormonal
 PT environments in animals of different reproductive states
 XX
 PS Example 1; Page 59-60; 85pp; English.
 XX
 CC This polypeptide is encoded by a newly isolated hormone-regulated
 CC gene, termed Repro-PC-1.0 (see AAV57327), isolated from prostate
 CC cancer cells. The polypeptide (calculated mol.wt. 48,070, pI 8.83)
 CC contains 2 copies of a 116-amino acid repeat that show homology
 CC to the C2 regulatory domain of calcium-dependent isoforms of
 CC protein kinase C, and to isoforms of synaptotagmin. Repro-PC1.0
 CC expression is specifically and differentially up-regulated in
 CC LNCaP tumour cells. The invention provides methods of identifying
 CC hormone-regulated traits in a cell. The methods involve
 CC cultivating the cell as a graft in 2 different hormonal
 CC environments and determining whether expression of the trait
 CC differs in the 2 grafts. The methods can be used to identify
 CC hormonally-regulated traits and hormonally-regulated genes for use
 CC as targets for therapeutic intervention in disease states,
 CC particularly cancers.
 XX
 SQ Sequence 425 AA;

Query Match 100.0%; Score 2201; DB 19; Length 425;
 Best Local Similarity 100.0%; Pred. No. 5.2e-196;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPYKFFVHLKGV 60
 DB 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPYKFFVHLKGV 60
 QY 61 DIYPENLNSKKKFGADDKNEVKKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 DB 61 DIYPENLNSKKKFGADDKNEVKKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 QY 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNERKAFVNNIKEARGL 180
 DB 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNERKAFVNNIKEARGL 180
 QY 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240
 DB 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240

QY 241 TTLSDFRFRSDIIGVLPISGLIELSEGKMLMREIIKRNVRKSSGRGELLISLCYOST 300
 DB 241 TTLSDFRFRSDIIGVLPISGLIELSEGKMLMREIIKRNVRKSSGRGELLISLCYOST 300
 QY 301 TNLTVVVLKARHLPKSDVSGLDPPYKVNLYHAKKRIKSKKTHVKKCTPNVAFNELFVF 360
 DB 301 TNLTVVVLKARHLPKSDVSGLDPPYKVNLYHAKKRIKSKKTHVKKCTPNVAFNELFVF 360
 QY 361 DIPCEGLEDISVEFLVLDSDRGRNEVIGQLVGLGAAAGTGGEHWKEICDYPRRQIAKWH 420
 DB 361 DIPCEGLEDISVEFLVLDSDRGRNEVIGQLVGLGAAAGTGGEHWKEICDYPRRQIAKWH 420
 QY 421 VLCDG 425
 DB 421 VLCDG 425

RESULT 3
 AAM93420
 ID AAM93420 standard; Protein; 431 AA.
 AAM93420;
 06-NOV-2001 (first entry)
 Human polypeptide, SEQ ID NO: 3040.
 Human; full length cDNA; cDNA synthesis; oligo-capping.

OS Homo sapiens.
 DE EP1130094-A2.
 PD 05-SEP-2001.
 XX 07-JUL-2000; 2000EP-0114089.
 XX 08-JUL-1999; 99JP-0194486.
 XX 11-JAN-2000; 2000JP-0118774.
 XX 02-MAY-2000; 2000JP-0183765.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 XX Wakamatsu A, Sugiyama I, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.
 XX N-PSDB; AAK94341.

PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX Claim 8; SEQ ID NO 3040; 1380pp + sequence listing; English.
 XX The invention relates to primers for synthesising full length cDNA
 XX clones. 830 cDNA molecules encoding a human protein have been
 XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 XX molecules have been determined. Primers for synthesising the full length
 XX cDNA are useful for clarifying the function of the protein encoded by
 XX the cDNA. The full length clones were obtained by construction of full
 XX length enriched cDNA libraries that were synthesised by the oligo-capping
 XX method. The primers enable the production of the full length cDNA easily
 XX without any special methods. The present sequence is a polypeptide
 XX encoded by a full length human cDNA of the invention.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 431 AA;
 XX Query Match 52.8%; Score 1162; DB 22; Length 431;
 XX Best Local Similarity 52.4%; Pred. No. 2.8e-99;
 XX Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;

QY 1 MADITTSREEFDEIPTVVGIFSAFLVETVS--LEAWICQCKQKSSKNKTPPYKFEVHLK 58
 DB 1 MADITTNIRPSFDSVPVAGLIGASLVVVCVSVTVFVWSCCHQQAERKKHNPYPKFIHMLK 60
 QY 59 GVDIYENLNSKKKF-----GADDKNEVKNKPAVPKNSIHLDLEKRDLDNGNFKTNLKP 113
 DB 61 GISIYETLSNKKKIIVRRDKDGPREGGRNLLVDAEAGLLSRD-----KDPRGPS 114
 QY 114 SPSDLNATPKL-----FLEGEKESVSPESLSKSTSLTSEEKQELGTLPFSLEYNERKA 169
 DB 115 SGSCIDQLPIKMDYGEELRSPITSITPGESK-TTSPSPSPEDVMLGSLTFSVDYNFPKA 173
 QY 170 FVNNIKEARGIPAMDEQSMSTDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTYGIP 229
 DB 174 LVVTIQEAHGLPVMDQTOGSDPYIKMTILPDKRHRVTRVLRKTLDPVDFDETFTYGIP 233
 QY 230 YTOIQELALHFTILSPDRFSRDDIIGEVLIPLSGIELSEGKMLMREIIKRNVRKSSGRG 289
 DB 234 YSOQLDLVHLFLVLSFDRFSRDDVIGEVVPLVAGVDPSTGKVLQTRDIIKRNIOKISRG 293
 QY 290 ELLISLCYQSTTNTLTIVVVLKARHLPKSDVSGLS--DPYKVNLYHAKKRIKSKKTHVKK 348
 DB 294 ELQVSLSYQFVQARMVTVVVLKARHLPKMDITGLSGNPYKVNLYHAKKRIKSKKTHVKK 353
 QY 349 TPNVAFNELFVDIPCEGLEDISVEFLVLDSDRGRNEVIGQLVGLA-AAGTGGGEHWKE 407
 DB 354 TLNPIFNESFIYDIPTDLLPDISIEFLVIDFDRTTKNEVVGRLILGAHVSVTASGAHWRE 413
 QY 408 ICYPRRQIAKWHVLC 424
 DB 414 VCESPRKPAKWHSLSE 430

RESULT 4
 AAM39577
 ID AAM39577 standard; Protein; 431 AA.
 XX AAM39577;
 XX 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 2722.

XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 XX peripheral nervous system; neuropathy; central nervous system; CNS;
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 XX leukaemia.

XX Homo sapiens.
 OS WO200153312-A1.
 PN 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX 09-JUL-2000; 2000US-0598042.
 XX 19-JUL-2000; 2000US-0620312.
 XX 03-AUG-2000; 2000US-0653450.
 XX 14-SEP-2000; 2000US-0662191.
 XX 19-OCT-2000; 2000US-0693036.
 XX 23-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.
 DR N-PSDB; AAI58733.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Example 4; SEQ ID NO 2722; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAI42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 XX Sequence 431 AA;
 SQ
 Query Match 52.8%; Score 1162; DB 22; Length 431;
 Best Local Similarity 52.4%; Pred. No. 2.8e-99;
 Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;
 Qy 1 MAPITTSREDFEIPTVVGIFSAFGLVFTVS--LFAMICCCQKSSKNKTPPYKVFHVLK 58
 Db 1 MAEITNIRPSDFVSPVAGLIGASVLVVCVTVFVWSCCHQQAQKHKNPYKFIHMLK 60
 Qy 59 GVDIYPENLNSKKKF-----GADDKNEVKNKPAVPKNSHLHLEKRLDNGNFPKTNLKP 113
 Db 61 GISIYPETLSNKKTKIKVRDDKPGREGRRLLVDAEAGLLSRD-----KDPGRPS 114
 Qy 114 SPSDLENATPKL----FLEGEKESVSPESLKSSTSLTSEKQKGLTLPFSLEYNPERKA 169
 Db 115 SGSCIDQPIKNDYGEELKSPITSPFGESK-TTSPSPDEEDVLMGLTFSVDYNFPPKA 173
 Qy 170 FVNIKEARGLPAMDEQSMTPYIKWTILPEKKHKVKTALVRLKTLDPAFDETTFYGP 229
 Db 174 LVVTIQEAHGLPMDDTQGSPIYIKWTILPKRHRVKVRLKTLDPVDETFYGP 233
 Qy 230 YTOIQELALHFFILSDFRSDRIIGEVJPLSGIELSEKGLMLNREIIRKNVRKSSGRG 289
 Db 234 YSQLQDLVLHLFLVLSDFRSDRDVIGEVVPLAGVDPSTCKVQLTRDIKRNQKCI SRG 293
 Qy 290 ELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLS-DPYVKVNLVHAKRKISKKTHVKKC 348
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 Qy 349 TPNVFNELFVDPIDCEGLEDISVRFVLDSRGRNEVIGQLVLGA-AAEGTGGEHWKE 407
 Db 354 TLNPFNFSFYDIPDLPLDISIEFLVDFDTRTKNEVGRVILGAHVSATGAHRE 413
 Qy 408 ICDYPRRQIAKHVLCID 424
 Db 414 VCESRPKPVAKHLSLE 430
 RESULT 5
 ID AAEI7500
 XX AAEI7500 standard; Protein; 431 AA.
 AC AAEI7500;
 XX
 DT 22-APR-2002 (first entry)
 XX Human secretion and trafficking protein-9 (SAT-9).

XX Human; secretion and trafficking protein-9; vesicle trafficking disorder;
 KW SAT-9; cystic fibrosis; diabetes mellitus; gastrointestinal disorder;
 KW Grave's disease; ulcerative colitis; cardiac disorder; hypertension;
 KW polymyositis; neurological disorder; Alzheimer's disease; dementia;
 KW depression; epilepsy; Tourette's disorder; cell proliferative disorder;
 KW cirrhosis; cancer; autoimmune disorder; inflammatory disorder; AIDS;
 KW acquired immune deficiency syndrome; Addison's disease; allergy; asthma;
 KW atherosclerosis; sickle cell anaemia; hyperglycaemia; transgenic animal;
 KW gene therapy; hypotensive; neurotropic; neuroprotective; antidepressant;
 XX anticonvulsant; neuroleptic; cytostatic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 16..37
 FT /label= Transmembrane_domain
 FT 158..285
 FT /label= C2_domain
 FT 287..419
 FT /label= C2_domain
 XX WO200202610-A2.
 XX 10-JAN-2002.
 XX 28-JUN-2001; 2001WO-US20704.
 XX 29-JUN-2000; 2000US-215465P.
 XX 10-OCT-2000; 2000US-239384P.
 XX 28-NOV-2000; 2000US-253639P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Lee EA, Lu Y, Lal P, Tang TY, Yue H, Wallia NK, Baughn MR, Das D;
 PI Ramkumar J, Tribouley CM, Lu DM, Rafalia A, Gandhi AR, Xu Y;
 PI Bandman O, Elliott VS, Nguyen DB, Burrill JD, Marcus GA;
 PI Zingler KA, Yao MG, Gururajan R, Ding L, Warren BA, Thangavelu K;
 PI Lee S;
 XX WPI; 2002-154727/20.
 DR N-PSDB; AAD28154.
 XX Novel human secretion and trafficking polypeptide, useful in diagnosis,
 PT prevention and treatment of vesicle trafficking, transport,
 PT neurological, autoimmune/inflammatory, and cell proliferative disorders
 PT -
 XX Claim 1; Page 120-121; 131pp; English.
 XX The present invention relates to human secretion and trafficking (SAT)
 CC proteins and their corresponding polynucleotides. SAT DNAs and proteins
 CC are useful for diagnosing, treating and preventing vesicle trafficking
 CC disorder (e.g. cystic fibrosis, diabetes mellitus, Grave's disease),
 CC gastrointestinal disorders (e.g. ulcerative colitis), cardiac disorders
 CC associated with transport (e.g. hypertension, polymyositis), neurological
 CC disorders associated with transport (e.g. Alzheimer's disease, dementia,
 CC depression, epilepsy, Tourette's disorder), cell proliferative disorders
 CC (e.g. cirrhosis, cancer), autoimmune or inflammatory disorders (e.g. AIDS
 CC (acquired immunodeficiency syndrome), Addison's disease, allergy, asthma,
 CC atherosclerosis) and other disorders associated with transport such as
 CC sickle cell anaemia and hyperglycaemia. SAT proteins are useful in a
 CC number of drug screening techniques and to analyse the proteome of a
 CC tissue or cell type. SAT DNAs are useful for creating knockin humanised
 CC animals or transgenic animals to model human diseases, in somatic or
 CC germline gene therapy, to generate a transcript image of a tissue or
 CC cell type, for detecting differences in the chromosomal location due
 CC to translocation, inversion, etc., among normal, carrier or affected
 CC individuals, and as hybridisation probes for mapping naturally occurring
 CC genomic sequences. The present sequence is human SAT-9 protein.
 XX Sequence 431 AA;

Query Match 52.4%; Score 1162; DB 23; Length 431;
 Best Local Similarity 52.4%; Pred. No. 2.8e-99;
 Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;

1 MAPITTSREEDFDEPTVVGIFSAFLVFTVS--LFAWICCCQKSSKSNKTPPKYKVVHLK 58
 1 MAEITNIRPSDFVSPVAGLIGASLVVCSVTVFVWSCCHQQAEEKKHNPYKFIHMLK 60
 59 GVDIYPENLNSKKKF-----GADKNEVKNPAVPKNSLHLDLEKRDNGNFPKTNLKP 113
 61 GISIYPETLSNKKKIIKVRDKDGPREGGRNLLVDAAEAGLLSRD-----KDPGRPS 114
 114 SPSDLENATPKL-----FLEGEKSVSPESLSKSTSLTSEKQKGLTGLTFFSLEYNFERKA 169
 115 SGSCIDQLPKMDYGEELRSPITSLTPGESK-TTSPSSPEEDVMLGSLTFSVDYNPPKKA 173
 170 FVNIKEARGLPAMDQSMSTDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFYFGIP 229
 174 LVVTIQEAHGLPVMDQDQSGSDPYIKMTILPKRHRVTRVLRKTLDPVDFETFTFYGIP 233
 230 YTOIQELALHFTILSFDRFRDDDIIGEVLIPLSGIELSEKGMNMREIIKRNVRKSSGRG 289
 234 YSLOQLDLVHLFVLSPDRFRDDVIGEVWVPLAGVDPSTGKVLTRDIIKRNQKISRG 293
 290 ELLISLCYSTNTLTVVVLKARHLPKSDVSGLS-DPYVKNVLYHAKKRIKSKKTHVKKC 348
 294 ELQVLSYQPVQAQRMVTVVLKARHLPKMDITGLSGNPYVKNVYGRKRIAKKTHVKKC 353
 349 TPNVAFNELFVFDIPCEGLEDISVEFLVLDSEGRSRNEVIGQLVLGA-AAEGTGGEHWKE 407
 354 TLNPIFNESFYDIPDTLLPDISTIEFLVIDPDRTTKNEVVGRLILGAHVSVTASGAHWRE 413
 408 ICYPRQIAKWHVLC 424
 414 VCESPRKPAKWHLSLSE 430

RESULT 6
 AAB92921 ID AAB92921 standard; Protein; 431 AA.
 AC AAB92921;
 26-JUN-2001 (first entry)
 Human protein sequence SEQ ID NO:11567.
 Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 Homo sapiens.
 EP1074617-A2.
 07-FEB-2001.
 28-JUL-2000; 2000EP-0116126.
 29-JUL-1999; 99JP-0248036.
 27-AUG-1999; 99JP-0300253.
 11-JAN-2000; 2000JP-0118776.
 02-MAY-2000; 2000JP-0183767.
 09-JUN-2000; 2000JP-0241899.
 (HELI-) HELIX RES INST.
 Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 WPI; 2001-318749/34.
 Primer sets for synthesizing polynucleotides, particularly the 5602
 full-length cDNAs defined in the specification, and for the detection
 and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -
 XX Claim 8; SEQ ID 11567; 2537pp + CD ROM; English.
 XX The present invention describes primer sets for synthesizing 5602
 full-length cDNAs defined in the specification. Where a primer set
 comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 to the complementary strand of a polynucleotide which comprises one of
 the 5602 nucleotide sequences defined in the specification, where the
 oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 of an oligonucleotide comprising a sequence complementary to the
 complementary strand of a polynucleotide which comprises a 5'-end
 sequence and an oligonucleotide comprising a sequence complementary to a
 polynucleotide which comprises a 3'-end sequence, where the
 oligonucleotide comprises at least 15 nucleotides and the combination of
 the 5'-end sequence/3'-end sequence is selected from those defined in
 the specification. The primer sets can be used in antisense therapy and
 in gene therapy. The primers are useful for synthesizing polynucleotides,
 particularly full-length cDNAs. The primers are also useful for the
 detection and/or diagnosis of the abnormality of the proteins encoded by
 the full-length cDNAs. The primers allow obtaining of the full-length
 cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 represent oligonucleotides, all of which are used in the exemplification
 of the present invention.

XX Sequence 431 AA;
 SQ Query Match 52.7%; Score 1159; DB 22; Length 431;
 Best Local Similarity 52.4%; Pred. No. 5.2e-99;
 Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;

QY 1 MAPITTSREEDFDEPTVVGIFSAFLVFTVS--LFAWICCCQKSSKSNKTPPKYKVVHLK 58
 DB 1 MAEITNIRPSDFVSPVAGLIGASLVVCSVTVFVWSCCHQQAEEKKHNPYKFIHMLK 60
 QY 59 GVDIYPENLNSKKKF-----GADKNEVKNPAVPKNSLHLDLEKRDNGNFPKTNLKP 113
 DB 61 GISIYPETLSNKKKIIKVRDKDGPREGGRNLLVDAAEAGLLSRD-----KDPGRPS 114
 QY 114 SPSDLENATPKL-----FLEGEKSVSPESLSKSTSLTSEKQKGLTGLTFFSLEYNFERKA 169
 DB 115 SGSCIDQLPKMDYGEELRSPITSLTPGESK-TTSPSSPEEDVMLGSLTFSVDYNPPKKA 173
 QY 170 FVNIKEARGLPAMDQSMSTDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFYFGIP 229
 DB 174 LVVTIQEAHGLPVMDQDQSGSDPYIKMTILPKRHRVTRVLRKTLDPVDFETFTFYGIP 233
 QY 230 YTOIQELALHFTILSFDRFRDDDIIGEVLIPLSGIELSEKGMNMREIIKRNVRKSSGRG 289
 DB 234 YSLOQLDLVHLFVLSPDRFRDDVIGEVWVPLAGADPSTGKVLTRDIIKRNQKISRG 293
 QY 290 ELLISLCYSTNTLTVVVLKARHLPKSDVSGLS-DPYVKNVLYHAKKRIKSKKTHVKKC 348
 DB 294 ELQVLSYQPVQAQRMVTVVLKARHLPKMDITGLSGNPYVKNVYGRKRIAKKTHVKKC 353
 QY 349 TPNVAFNELFVFDIPCEGLEDISVEFLVLDSEGRSRNEVIGQLVLGA-AAEGTGGEHWKE 407
 DB 354 TLNPIFNESFYDIPDTLLPDISTIEFLVIDPDRTTKNEVVGRLILGAHVSVTASGAHWRE 413
 QY 408 ICYPRQIAKWHVLC 424
 DB 414 VCESPRKPAKWHLSLSE 430

RESULT 7
 AAM41363 ID AAM41363 standard; Protein; 486 AA.
 XX AAM41363;
 XX 22-OCT-2001 (first entry)
 DT

Sequence 474 AA;
 Query Match 34.4%; Score 757; DB 22; Length 474;
 Best Local Similarity 38.2%; Pred. No. 1.6e-61;
 Matches 179; Conservative 82; Mismatches 137; Indels 70; Gaps 14;
 14 IPTVVGIFSAFGLVFTVSLFAWLCQ-----RKSSKSNKTPPYKFF----- 54
 16 VFALIGLTA---AVLSSVACICARQMLRNKKQSDHASFPPQTRPFAVSPSQP 71
 55 -HVLKGVDPYIPENLNSKFKGADKNEVKNKPAVPKN-----SLHLDLEKRLDNG 103
 72 PHYLK---SPSTGCKQKGLLSPMDQOSTPIAQNPKVYSEEGDGAQHAQQ-----NG 124
 104 N----FPKTNLPGSPDLENATPKLLEGEKE-SVSPESLSKSTSLTSEKQKGLTFL 158
 125 NQLTVVDGNGKLSLHNSLHSHSVETIANGSVTTILDHSLTNGKELTVTDQYKGLTIY 184
 159 FSLYNFERKAFVNNKEARGLPADEQSWT-----SPYIKNTILPEKKH 204
 185 FKRLYLAERNALMVSIRCRGLPKCGSSGTGDIPTGMNGRTQAATDPYVKLQLLPDKQH 244
 205 KYKTRVLRKTLPADETFEYGIPTQIOELALHFTLSPDRESRDDIIGEVLIPLSGI 264
 245 KYKTRVVRNRPVYDEDFYGLNMDLQNMSLHFVILSPDRYSDRDVIGEVVCELTSI 304
 265 E---LSEGMKLMNREIKRNVK-KSSGRGELLISLCYQSTNTTLTVVVKARHLPKSDVS 320
 305 EIGDISKEALSISKEITQPSRLKTRAQGRGELLISLCWPAAGRLTVLLKARNLPMDVT 364
 321 GLSDPYVKNVLYHAKRKISKKTHVKCTNPVNFELVFEDIP-CEG----LEDISVFL 375
 365 GLADPVVKIYLLNGQRIAKKTHVKRTLSPVNESAFAFDIPAAEGAGASLEGVSLML 424
 376 VLDSEGRSNEVIGQLVGLAA-ABGTGGEHWKEICDYPRIQIAKHWL 422
 425 LLDMDRVTKNEVIGRLGLGPNSSSTALNHNVEVNCSPRQIAEWHKL 472

RESULT 9
 ID ABG70275
 ABG70275 standard; Protein; 403 AA.
 AC ABG70275;
 XT 05-NOV-2002 (first entry)
 DE Human Synaptotagmin-like protein #2.
 KW Human; NOVX; pathological condition; NOVX-associated disorder;
 KW Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
 KW pancreatitis; obesity; diabetes; autoimmune disease; infertility;
 KW renal artery stenosis; interstitial nephritis; glomerulonephritis;
 KW polycystic kidney disease; cataract; Alzheimer's disease; cancer;
 KW acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;
 KW congenital heart defect; scleroderma; endometriosis; haemophilia;
 KW dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;
 KW multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
 KW acne; wound; asthma; human disease; calpain; epain; zinc finger;
 KW low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;
 KW serine protease TLSP; mitogen activated protein kinase kinase-2;
 KW glypican-2 precursor; thymosin beta-10.
 OS Homo sapiens.
 GN WO200255702-A2.
 IN 18-JUL-2002.
 PD 26-OCT-2001; 2001WO-US50925.
 PF 26-OCT-2000; 2000US-243320P.
 PR 26-OCT-2000; 2000US-243592P.

26-OCT-2000; 2000US-243642P.
 27-OCT-2000; 2000US-243681P.
 27-OCT-2000; 2000US-243863P.
 31-OCT-2000; 2000US-244433P.
 01-NOV-2000; 2000US-244995P.
 01-NOV-2000; 2000US-245029P.
 02-NOV-2000; 2000US-245293P.
 02-NOV-2000; 2000US-245315P.
 02-NOV-2000; 2000US-245316P.
 19-JAN-2001; 2001US-262994P.
 15-FEB-2001; 2001US-269056P.
 02-MAR-2001; 2001US-272923P.
 15-MAR-2001; 2001US-276565P.
 07-SEP-2001; 2001US-318119P.
 (CURA-) CURAGEN CORP.
 Gargolli EA, Spytek KA, Casman S, Blalock A, Li L;
 Vernet CAM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S;
 Malyankar U, Stone D, Millet I, Smithson G, Gunther E, Padigaru M;
 Taupier RJ, Anderson D;
 WPI: 2002-590673/63.
 N-PSDB; ABK51682.
 Isolated NOVX polypeptides and nucleic acid molecules useful for
 treating, preventing, diagnosing and researching pathological
 conditions in humans with a NOVX-associated disorders, e.g. cancer,
 stroke or Alzheimer's disease -
 Claim 1; Page 46; 236pp; English.
 The present invention relates to a new polypeptide that comprises any of
 17 fully defined sequences of 43-990 amino acids given in the
 specification. The NOVX polypeptide, nucleic acid and antibody of the
 invention are useful for treating or preventing a pathological condition
 in humans with a NOVX-associated disorder, e.g. Von Hippel-Lindau
 syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity,
 diabetes, autoimmune disease, renal artery stenosis, interstitial
 nephritis, glomerulonephritis, polycystic kidney disease, cataract,
 Alzheimer's disease, atherosclerosis, hypertension, congenital heart
 defects, scleroderma, endometriosis, haemophilia, dementia, stroke,
 Parkinson's disease, Huntington's disease, epilepsy, multiple
 sclerosis, anxiety, pain, leukaemia, hypothyroidism, psoriasis, acne,
 wounds and asthma. They are also useful for the manufacture of a
 medicament for treating a syndrome associated with a human disease,
 specifically a NOVX-associated disorder. They may also be useful in
 therapeutic applications including protein therapy, as small molecule
 drug targets, as antibody targets, as diagnostic and/or prognostic
 markers, in gene therapy, as research tools and in tissue regeneration.
 The present amino acid sequence represents one of the 17 novel proteins
 of the invention.
 Sequence 403 AA;
 Query Match 28.3%; Score 622.5; DB 23; Length 403;
 Best Local Similarity 36.2%; Pred. No. 4.1e-49;
 Matches 153; Conservative 71; Mismatches 128; Indels 71; Gaps 11;
 27 VFTVSL-----FAWIC-CQKSSKSNKTPPYKFVHLKGVDPYIPENLNSKFKGADD-- 77
 23 IITVLSVTVVLGCLCHWCQKGLKRYK-----NSLETVGTPDSG 62
 78 -----KNEVK-----NKPAVKNLSLHLDLEKRLDNGNEPKTNLPGSPDLENATPK 124
 63 RGRSEKAIKLPAAGKAVNTAPVPGQTPHDSRR-----TEPRS-----SVSLVN---- 109
 125 LFLEGEKESVPSLSKSTSLTSEE-----KQKLGTLFFSLFYNFERKAFVNNKEARG 179
 110 -----SLTSEMMLSPGSEEDAEHGCSEENLGRIOFSVGNFQESTLTVKIMKAOE 161
 180 LPAMDEQMSDPIYIKMTILPEKKHKVTRVLRKTLPADETFEYGIPTQIOELALH 239

28-JUN-2000; 2000US-0214886.
 30-JUN-2000; 2000US-0215135.
 07-JUL-2000; 2000US-0216647.
 07-JUL-2000; 2000US-0216880.
 11-JUL-2000; 2000US-0217487.
 11-JUL-2000; 2000US-0217496.
 14-JUL-2000; 2000US-0218290.
 26-JUL-2000; 2000US-0220963.
 26-JUL-2000; 2000US-0220964.
 14-AUG-2000; 2000US-0224518.
 14-AUG-2000; 2000US-0224519.
 14-AUG-2000; 2000US-0225213.
 14-AUG-2000; 2000US-0225214.
 14-AUG-2000; 2000US-0225266.
 14-AUG-2000; 2000US-0225267.
 14-AUG-2000; 2000US-0225268.
 14-AUG-2000; 2000US-0225270.
 14-AUG-2000; 2000US-0225447.
 14-AUG-2000; 2000US-0225757.
 14-AUG-2000; 2000US-0225758.
 14-AUG-2000; 2000US-0225759.
 18-AUG-2000; 2000US-0226279.
 22-AUG-2000; 2000US-0226681.
 22-AUG-2000; 2000US-0226688.
 22-AUG-2000; 2000US-0227182.
 23-AUG-2000; 2000US-0227009.
 30-AUG-2000; 2000US-0228924.
 01-SEP-2000; 2000US-0229287.
 01-SEP-2000; 2000US-0229343.
 01-SEP-2000; 2000US-0229344.
 01-SEP-2000; 2000US-0229345.
 05-SEP-2000; 2000US-0229509.
 05-SEP-2000; 2000US-0229513.
 06-SEP-2000; 2000US-0230437.
 06-SEP-2000; 2000US-0230438.
 08-SEP-2000; 2000US-0231242.
 08-SEP-2000; 2000US-0231243.
 08-SEP-2000; 2000US-0231244.
 08-SEP-2000; 2000US-0231413.
 08-SEP-2000; 2000US-0231414.
 08-SEP-2000; 2000US-0232080.
 08-SEP-2000; 2000US-0232081.
 12-SEP-2000; 2000US-0231968.
 14-SEP-2000; 2000US-0232397.
 14-SEP-2000; 2000US-0232398.
 14-SEP-2000; 2000US-0232399.
 14-SEP-2000; 2000US-0232400.
 14-SEP-2000; 2000US-0232401.
 14-SEP-2000; 2000US-0233063.
 14-SEP-2000; 2000US-0233064.
 14-SEP-2000; 2000US-0233065.
 21-SEP-2000; 2000US-0234223.
 21-SEP-2000; 2000US-0234274.
 25-SEP-2000; 2000US-0234997.
 25-SEP-2000; 2000US-0234998.
 26-SEP-2000; 2000US-0235484.
 27-SEP-2000; 2000US-0235834.
 27-SEP-2000; 2000US-0235836.
 29-SEP-2000; 2000US-0236327.
 29-SEP-2000; 2000US-0236367.
 29-SEP-2000; 2000US-0236368.
 29-SEP-2000; 2000US-0236369.
 29-SEP-2000; 2000US-0236370.
 02-OCT-2000; 2000US-0236802.
 02-OCT-2000; 2000US-0237037.
 02-OCT-2000; 2000US-0237038.
 02-OCT-2000; 2000US-0237039.
 02-OCT-2000; 2000US-0237040.
 13-OCT-2000; 2000US-0239935.
 13-OCT-2000; 2000US-0239937.
 20-OCT-2000; 2000US-0240960.
 20-OCT-2000; 2000US-0241221.
 20-OCT-2000; 2000US-0241785.

20-OCT-2000; 2000US-0241786.
 20-OCT-2000; 2000US-0241787.
 20-OCT-2000; 2000US-0241808.
 20-OCT-2000; 2000US-0241809.
 01-NOV-2000; 2000US-0241826.
 01-NOV-2000; 2000US-0244617.
 08-NOV-2000; 2000US-0246474.
 08-NOV-2000; 2000US-0246475.
 08-NOV-2000; 2000US-0246476.
 08-NOV-2000; 2000US-0246477.
 08-NOV-2000; 2000US-0246478.
 08-NOV-2000; 2000US-0246523.
 08-NOV-2000; 2000US-0246524.
 08-NOV-2000; 2000US-0246525.
 08-NOV-2000; 2000US-0246526.
 08-NOV-2000; 2000US-0246527.
 08-NOV-2000; 2000US-0246528.
 08-NOV-2000; 2000US-0246532.
 08-NOV-2000; 2000US-0246609.
 08-NOV-2000; 2000US-0246610.
 08-NOV-2000; 2000US-0246611.
 08-NOV-2000; 2000US-0246613.
 17-NOV-2000; 2000US-0249207.
 17-NOV-2000; 2000US-0249208.
 17-NOV-2000; 2000US-0249209.
 17-NOV-2000; 2000US-0249210.
 17-NOV-2000; 2000US-0249211.
 17-NOV-2000; 2000US-0249212.
 17-NOV-2000; 2000US-0249213.
 17-NOV-2000; 2000US-0249214.
 17-NOV-2000; 2000US-0249215.
 17-NOV-2000; 2000US-0249216.
 17-NOV-2000; 2000US-0249217.
 17-NOV-2000; 2000US-0249218.
 17-NOV-2000; 2000US-0249244.
 17-NOV-2000; 2000US-0249245.
 17-NOV-2000; 2000US-0249264.
 17-NOV-2000; 2000US-0249265.
 17-NOV-2000; 2000US-0249297.
 17-NOV-2000; 2000US-0249299.
 17-NOV-2000; 2000US-0249300.
 01-DEC-2000; 2000US-0250160.
 01-DEC-2000; 2000US-0250391.
 05-DEC-2000; 2000US-0251030.
 05-DEC-2000; 2000US-0251988.
 05-DEC-2000; 2000US-0256719.
 06-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
 08-DEC-2000; 2000US-0251858.
 08-DEC-2000; 2000US-0251869.
 08-DEC-2000; 2000US-0251989.
 08-DEC-2000; 2000US-0251990.
 11-DEC-2000; 2000US-0254097.
 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-581633/65.

N-PSDE; ABK43584.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 9; SEQ ID No 772; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative

tranquilliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory;
anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;
metabolic disorder; obesity; infectious disease; Alzheimer's disease;
anorexia; neurodegenerative disorder; Parkinson's disease; obesity;
immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
metabolic syndrome X; wasting disorder; cancer; neurological disorder;
epilepsy; stroke; mental disorder; schizophrenia disorders; goiter;
vesicular transport; cystic fibrosis; gastrointestinal disorder;
diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
multiple sclerosis; rheumatoid arthritis; AIDS; transgenic animal;
gene therapy.

Unidentified.

WO200246409-A2.

13-JUN-2002.

06-DEC-2001; 2001WO-US46586.

06-DEC-2000; 2000US-251660P.

12-DEC-2000; 2000US-255029P.

08-JAN-2001; 2001US-260326P.

24-JAN-2001; 2001US-263800P.

20-FEB-2001; 2001US-269942P.

24-APR-2001; 2001US-286183P.

20-AUG-2001; 2001US-313627P.

12-SEP-2001; 2001US-318712P.

(CURA-) CURAGEN CORP.

Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM;

Tchernev VT, Vernet CAM, Spytek KA, Shenoy SG, Alsbrook JP;

Edinger S, Peyman JA, Stone DU, Ellerman K, Gangolli EA;

Boldog FL, Colman SD, Eisen AJ, Liu X, Padigaru M, Spaderna SK;

Zerhusen BD;

WPI; 2002-547774/58.

N-PSDB; A8T05458.

Novel isolated polypeptide, designated NOVX, useful for treating or

preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and

metabolic, neurodegenerative, immune and hematopoietic disorders -

Claim 1; Page 53; 421pp; English.

The invention relates to an isolated polypeptide, designated NOVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polynucleotide or an antibody created from the protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder, or for treating or preventing a NOVX-associated disorder in a subject, preferably human. The isolated protein, its encoding polynucleotide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorder, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with chronic diseases, and cancer. The isolated protein, its encoding polynucleotide or an antibody created from the protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, mental disorders including mood, anxiety, schizophrenic disorders, disorders of vesicular transport such as cystic fibrosis, diabetes mellitus, goiter, gastrointestinal disorders including ulcerative colitis, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynucleotide of the invention can be used to treat disorders by gene therapy. This sequence represents one of the isolated NOVX proteins of the invention.

Sequence 523 AA;

Query Match	27.7%; Score 609; DB 23; Length 523;
Best Local Similarity	34.6%; Pred. No. 1.1e-47;
Matches 159; Conservative	73; Mismatches 155; Indels 72; Gaps 16;
QY	20 IFSAPGL-VFTVSLFA-WICQKSSKSNKTPPYKVFHVLKGVDPYENLNS--KKKFGA 75
DB	60 VVSFCGLLVSLFVFWKLC-----WPCWKSFPVTSNITLPOSISAPTEVET 110
QY	76 DDKNEVK--NKPAVPKNSLHLDLEKRDNGNFP---KTNLK-----PGSP 115
DB	111 EKKEIKENEKPAV--KAIEPAIKISHTSPDIPAETVQTKALKEHLIKHARVQRIEPTSS 168
QY	116 S-----DLENATPKLFLEGEKES-----VSPSLKSSSTSLTSEKQEK 153
DB	169 TRHSSPRHLPRQMVSSVDFSMGTPEVLQRGTTTSGRIKPELYKOK-SVDSGQNQE 227
QY	154 ----LGTFLFSLEYNFERKAFVNNIKEARGLPADEQSWTSDPYIKMTILPKKHVKTR 209
DB	228 DVKICGKLNFTLQDYENELLVVKKIKALDLPKADFTG-TSDPYVVMYLLPDRKKKQFPR 286
QY	210 VLKRTLDPAFDETFYGIPIYTOIQELALHFTILSDFRSDRDIIGEVILPLSGIELSG 269
DB	287 VHRKTLNPLFDETFQP-PVAYDQLSNRKLFHSVYDFRFSRDMIGEVLID----NLFEV 341
QY	270 KMLMREIIRKRVN---KSSGRGELLISLCYQSTTNTLTIVVVKARHLPKSDVSLSDP 325
DB	342 SLSREATVWKDIHCATTESIDIGEIMFSLCYLPTAGMTLTVIKRNLKAMDITGSSDP 401
QY	325 YKVNLYHAKRISKKTHVVKCTPNNAVFNELFVFDIPCEGLEDISVFLVLDSEGRSN 385
DB	402 YKVSILMCEGRRLKRTTKTKNTLNPVNEAIIIFIPPENVDQVSLSAVMVDYDRVGHN 461
QY	386 EVTGQVLVLGAAGTGGHKKWKEICDYPKQIAKWHVLCDD 424
DB	462 EVTGVCRTGDAEGLGRDHWNEMLAYHRKPTTHWHPLLE 500

RESULT 14

AAO19183

ID AAO19183 standard; protein; 533 AA.

AC AAO19183;

DT 27-NOV-2002 (first entry)

XX Human neurotransmission-associated protein NTRAN6.

XX Human; neurotransmission-associated protein; NTRAN; autoimmune disorder;
inflammatory disorder; cancer; cardiovascular disorder; infection;
neurological disorder; metabolic disorder; immunomodulatory; nootropic;
neuroprotective; antiinflammatory; cytostatic; cardiac; gene therapy.

XX Homo sapiens.

XX WO200266646-A2.

PN 29-AUG-2002.

XX 15-FEB-2002; 2002WO-US04536.

XX 16-FEB-2001; 2001US-269748P.

PR 11-MAY-2001; 2001US-290524P.

PR 19-OCT-2001; 2001US-343742P.

XX (INCY-) INCYTE GENOMICS INC.

XX Duggan BM, Honchell CD, Ison CH, Thangavelu K, Lu DAM, Baughn MR;
Lal PG, Yue H, Tang YT, Warren BA, Lee EA, Griffin JA;
Forsythe IO, Wallia NK;

XX WPI; 2002-674945/72.

DR N-PSDB; AAL49656.

Search completed: February 20, 2004, 13:12:49
Job time : 48 secs